Mapping the impact of invasive alien species on mountain ecosystems

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BABVE

Bernat Claramunt-López compiled the published scientific articles necessary for the subsequent data extraction, partially reviewed these literature, supervised the development of the approach, and reviewed the manuscript. My contribution to this study began in September 2020. I downloaded and partially reviewed the compiled articles, extracted data from the literature, reviewed the collected data, scored species to calculate the impact, analysed and processed the datasets, performed GIS and statistical analysis, and wrote the manuscript.

The manuscript is formatted according to Science of the Total Environment guidelines.

ABSTRACT

The aim of this study is to map and evaluate the impact of invasive alien species in different mountainous regions of the world, to identify high-impacted areas and find out which phyla have been the most problematic. According to our hypothesis, the biogeographic location where the impact occurs, its IASs richness and the average elevation could explain the variability of the cumulative impact values (CIMPAL scores) across terrestrial mountain systems. We adapted the conservative additive model of Katsanevakis *et al*. (2016) and applied it at a regional scale. We standardized cumulative impact values per cell area and the resulting StCIMPAL scores showed strong spatial heterogeneity. Impacted cells appeared to be aggregated and some impacted hotspots could be differentiated, especially in the Alps, the French Massif Central, the Appalachian Mountains, the Rocky Mountains, Taiwan, the Cape Ranges, the Great Dividing Range, and the Southern Alps. Some heavily impacted areas partially coincided with IASs-rich zones. Despite this, we found impacted cells scattered throughout all the study area. We then estimated the effect of *average elevation*, *IASs richness* and *great mountain ranges* (*GMRs*) on *StCIMPAL scores* by fitting Tweedie's compound Gamma-Poisson generalized linear models with a log link function. We found clear patterns between StCIMPAL scores and both elevation and IASs richness, as well as significant interactions with GMRs. Post-hoc comparisons showed significant differences among GMRs. We also identified the low-impacted and the high-impacted areas. Finally, we estimated the most problematic IASs by quantifying its relative impact values, although we obtained different results depending on the indicator used; only *Adelges tsugae*, *Cervus elaphus*, *Impatiens glandulifera* and *Robinia pseudoacacia* appeared in more than one. Our work shows the altitudinal patterns that modulate the cumulative impacts of invasive alien species in mountain ecosystems, revealing the different relationships between cumulative impact scores and IASs richness among terrestrial biogeographic regions.

KEYWORDS

Biological invasions / Cumulative impacts / Great mountain ranges / Invasive alien species (IASs) / Mapping / Mountain ecosystems

1. INTRODUCTION

A well-documented type of ecological impact is the effect of invasive alien species (IASs). They are defined as species, subspecies, or lower taxa that occur outside their past or present natural area and that have become problematic in the regions where they are considered non-native (Dudgeon et al., 2006; Strayer, 2010; Bellard et al., 2016; Maxwell et al., 2016; IUCN, 2020). Biological invasions are complex and consist of a sequential transition of stages which can fail or succeed (Sakai et al., 2001). The phases are transport and introduction (accidental or intentional), colonization, establishment and spread; the cycle closes when these species facilitate or cause new invasion episodes (Mack et al., 2000; Walther et al., 2009). In this context, expansions induced by human action are also considered biological invasions (Acevedo and Cassinello, 2009).

IASs have many different impacts on natural systems. Once established, IASs can significantly affect the structure of recipient habitats and the populations of native species that live there – by altering genetic compositions and extinction probabilities. This, in the long run, can condition the diversity and richness of invaded communities. IASs can also bring about changes in many other ecological processes, such as behavioural patterns, disturbance regimes, food webs, hydrology, nutrient cycles, and productivity (Brooks et al., 2004; Hendrix et al., 2008; Suarez and Tsutsui, 2008; Kenis et al., 2009; Winter et al., 2009; Vilà et al., 2011; Pyšek et al., 2012; Ricciardi et al., 2013). All of them harm ecosystem services, human health, livelihoods and/or food security, and can end up impacting the economy and the well-being of the society (IUCN, 2020). IASs have repercussions on a global scale, which is why several multilateral environmental agreements (MEA) explicitly address this issue: for example, the Convention on Biological Diversity (CBD; Essl et al., 2020a), the International Plant Protection Convention (Lopian, 2003), and the United Nations Sustainable Development Goals (specifically, the SDG 15 "Land on Land" from 2030 Agenda for Sustainable Development; United Nations, 2015), among others (Shine, 2007; Ormsby and Brenton-Rule, 2017). At the same time, there are initiatives (i.e., the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services), regulations (e.g., EU Regulation 1143/2014; European Union, 2014), conservation strategies (e.g., EU Biodiversity Strategy for 2030; European Commission, 2021) and global networks of experts (e.g., IUCN SSC Invasive Species Specialist Group) that provide information as support for practitioners, policy makers, and decision takers (Pagad et al., 2015; Magliozzi et al., 2020).

In general, governments, scientists, and conservation organizations view IASs as undesirable elements in natural ecosystems (Pyšek et al., 2020). Although IUCN recommends a cross-cutting approach to managing the environmental and socio-economic issues arising from IASs, many countries have failed to implement cooperative actions to address them – mainly because there is a lack of efficient communication between administrations, landowners, and other sectors of the society (Elliston and Beare, 2005; IUCN, 2020). The scale of costs associated with IASs is still not well understood, but their direct impacts and management are estimated to cost to the global economy billions of US dollars a year (Pimentel et al., 2001; Bradshaw et al., 2016; Courtois et al., 2018; IUCN 2021). For example, significant amounts of resources are spent on measures to prevent and control the effects of IASs, including biosecurity (which is considered the most cost-effective way to deal with IASs), early detection, monitoring or early eradication actions (Hulme, 2009; Katsanevakis et al., 2013; IUCN 2020).

The spread of IASs in the mountainous regions of the world poses a serious threat to their ecosystems, which are recognized for their high ecological, economic, aesthetic, social and cultural value (Sayre et al., 2018; Siniscalco and Barni, 2018). Although mountains have traditionally been considered stable systems in the face of the effects of IASs, several phenomena as climate change, land use shifts, and rising rates of new introductions could amplify their impact (Richardson et al., 1996; Rouget et al., 2003; Walther et al., 2009; McDougall et al., 2011; Essl et al., 2020b). This is specially worrying because mountains are biodiversity hotspots, hosting many endemic species, and with rich and different flora, compared to the surrounding lowlands areas (Körner, 2004; Chape et al., 2009; Siniscalco and Barni, 2018; Rahbek et al., 2019).They are also key pieces for terrestrial life, since they provide much of the world's freshwater supply and are closely related to the climate at all scales (Bailey, 2009); they also function as geographic barriers and biological corridors, which can influence – among other variables – gene flow (Zalewski et al., 2009) and distributional shifts (Knowles and Massatti, 2017). Mountains provide important ecosystem services for agriculture and forestry, such as grazing activities, related food production, or the extraction of timber and non-timber forest products; they also allow the realization of sports and touristic, recreational, and spiritual activities (Sayre et al., 2018; Siniscalco and Barni, 2018). Millions of people derive some or all their livelihood from mountain systems, so human dependence on their habitats is considerable (FAO, 2015; Körner et al., 2017; Sayre et al., 2018). Mountain conservation has been a globally recognized priority policy since its inclusion in Chapter 13 of Agenda 21 at the 1992 Rio Conference (Rio Conference, 1992), and is currently also included in the SDGs 6 “Clean Water and Sanitation” and 15 “Life on Land” (United Nations, 2015; Sayre et al., 2018).

An effective and sustainable management of mountains requires an increasingly detailed knowledge of their complexity (Sayre et al., 2018). Cumulative impact mapping is used to assess the effects associated with activities and phenomena that occur in the natural environment (Smit and Spaling, 1995), and its methodology integrates spatial information, which is useful in understanding geographical patterns at different scales. Thus, it is a tool for the management and conservation of biodiversity that allows to define and prioritize explicit operational objectives. These analyses are abundant in the scientific literature, but most of them are focused on marine environments (Halpern et al., 2008; Halpern et al., 2009; Halpern and Fujita, 2013; Halpern et al., 2015; Ban et al., 2010; Micheli et al., 2013; Andersen et al., 2015; Katsanevakis et al., 2016; Halpern et al., 2019; Hansen, 2019; Hammar et al., 2020, and others); whereas few have applied this technique in terrestrial environments or inland waters (Johnston, 1994; Johnston et al., 1988; Johnston et al., 1990; Roscioni et al., 2013; Turbelin et al., 2017; Allan et al., 2019; Gao et al., 2021; Mayani-Parás et al., 2021). Similarly, most publications on IASs deal with case studies in specific locations – and involve one or a few taxa in one or a few habitats (Katsanevakis et al., 2016). To have a more general view, Katsanevakis et al. (2016) developed a quantitative and standardized methodology which allowed them to map the cumulative impacts of IASs on the marine environments of the Mediterranean Sea. Since then, other researchers have presented similar works (e.g., Liversage et al., 2019; or Magliozzi et al., 2020), expanding our knowledge about this type of environmental impact, and have strengthened the validity of the CIMPAL score (Cumulative IMPacts of invasive ALien species) as a tool for impact analysis (Katsanevakis et al., 2016).

The aim of this study is (1) to map and evaluate the documented impacts of IASs (only animals and plants) in different mountainous regions of the world, (2) to identify high-impacted areas, and (3) to assess which phyla are the most problematic. According to our hypothesis, the relationship between cumulative impact scores and IASs richness in terrestrial mountain systems should differ among biogeographic regions, and the average elevation ought to have a variable effect depending on the great mountain range where the impact occurs.

2. MATERIALS AND METHODS

2.1. Data curation

2.1.1. Raster and vector layers preparation

First, we used and adapted several raster and vector layers (Appendix A1); all these processes were performed with QGIS 3.16.4. Hannover (QGIS Development Team, 2021) and RStudio 1.3.1093 (R Core Team, 2021):

We grouped the mountains of the world (in polygon format) from GMBA (Körner et al., 2017) into 20 great mountain ranges (henceforth, GMRs; Table A1) – following the previous framework of Grêt-Regamey and Weibel (2020); to delimit these groups, we also consulted geomorphological maps from IAS PMF (www.pmfias.com). Given that we created the GMRs to extrapolate the impacts associated with the IASs included in this study, we listed the countries that intersected with the areas of each group (hereinafter, C-GMRs; Table A2) – as we needed this information to obtain GBIF occurrence data (see below; section *2.1.3.2. Obtaining GBIF occurrence data*). However, we did not use 5 GMRs (Atlas, Madagascar, Tropical East Asia Ranges, Greenland, and Amazonian Rainforest - The Pampas), since there were no IAS inventoried that would generate any documented impact.

We created a grid layer with cells of 0,09 x 0,09 geographical degrees (GRID layer) and clipped it for each GMR (Appendix A2). We also clipped by extend and transformed to vector points the global land cover raster (≈1 sq. Km/pixel, *Beta-release Version 1.0.*; Latham et al., 2014) and the DEM raster (*ETOPO5*; NOAA, 1988) – so we got several subsets of these layers corresponding to the different GMRs (Appendix A3). We used the DEM filtered information to determine the average elevation value per grid cell (Appendix A4); for this purpose, we used R packages *dplyr* (*v1.0.7.*; Wickham et al., 2021) and *sf* (Pebesma, 2018).

2.1.2. Mountain IASs inventory: assessing IASs in the world's mountain systems

2.1.2.1. Bibliographic data and synthesis

We compiled published scientific literature to create an inventory of IASs associated with impacts on the world's mountain systems. In addition, we selected some of these species using various inclusion criteria (see below).

The bibliographic collection was made in September 2020, through the ISI Web of Knowledge academic database (www.webofknowledge.com). We restricted research into the areas of environmental sciences, ecology, zoology, and biodiversity conservation, and included all peer-reviewed articles in English that contained in the title, abstract or keywords, any of these terms: (*alien* or *exotic* or *invasive* or *invasion* or *non-native*) AND (*impact**) AND (*mountain** or "*mountain ecosystems"*). We did not consider grey literature or non-English language publications.

The search returned 392 results, that we sorted by relevance, and selected the first 245 titles. We then structured a list with the basic information of each publication, which included at least the reference and the abstract. The aim was to review this information so that we could decide which selected articles could provide us with data for the creation of the IASs inventory. Through several readings and with the help of a table for information extraction, we selected 173 publications (70%) – which we considered valid for the next round of review. These articles clearly presented impacts associated with IASs in terrestrial environments or included content that we found potentially relevant. The 72 publications we excluded in this first filtering (30%) were discarded because: (1) they dealt with other fields of ecology, (2) they were exclusively methodological or were conceptual revisions, (3) they listed IASs but did not describe any associated impact, or (4) did not include specific case studies.

For the second selection process, we downloaded the articles that has passed the first round of validation; and we read, in detail, the full texts (including figures, tables, and supplementary material). At this point, we considered that only publications that met the following inclusion criteria were appropriate: (1) they had to show some kind of ecological impact, and this had to be well described; (2) impact estimates had to be associated with more than one individual; (3) individuals had to be registered at the species or genus level, and could only be from the Animalia or Plantae kingdoms; (4) these species or genera had to be considered exotic or invasive in the study area; (5) the impact described had to be associated with some type of habitat, or more than one; (6) the article had to contain enough information to correctly define each affected habitat, and (7) the area where the impact occurred had to be mountainous. Out of the 173 publications, 106 were considered suitable (Table B1).

From each article, we collected the following data: (1) the year of publication and the name of the first author; (2) the scientific name of the IAS; (3) the names of the main taxonomic categories to which it belongs: gender, family, class, and kingdom; (4) the origin or native distribution range; (5) the country and continent where the impact was described; (6) the toponyms of the study sites, in great detail; (7) the toponym of the invaded mountain, mountainous region, or mountain range; (8) the affected habitat or habitats; (9) the type of study used, based on the classification of Katsanevakis et al. (2016); (10) the strength of evidence: limited < medium < robust (Katsanevakis et al., 2016); (11) the type of associated impact; (12) the magnitude of the impact: minimal < minor < moderate < major < massive (Katsanevakis et al., 2016), and (13) other observations. The 106 articles consulted corresponded to 101 different authors and had been published between 2000 and 2019 (over 20 years). We assigned an internal identification number to each publication, with a range between 001 and 106 (Table B2).

In most publications it was clearly stated: (1) the scientific name of the IAS – and often the common name; (2) the country where the impact was described, and (3) accordingly, the continent. However, some articles contained incomplete, ambiguous, out-of-print, or inaccurate information, or had spelling and nomenclature errors. For example, higher taxonomic categories or native distribution ranges in some cases were not indicated. For this reason, we consulted additional literature, open/public databases and/or online resources.

The descriptions of the study sites were variable among publications: some sampling had been carried out at very specific points – such as experimental stations – while in others the sampling range occupied large areas. In addition, some impacts were described in heterogenous landscapes, formed by mountainous and non-mountainous areas. We noted only the locations that were on mountainous terrain, and to distinguish it we consulted in detail the text and tables of each publication. In ambiguous cases, we searched for the toponyms of the study sites or their geographical coordinates through Google Earth and decided – through visual assessment – the type of terrain on which they occurred.

We also resorted to specific procedures in order to locate the mountains, mountainous regions or mountain ranges impacted in those publications in which it was not clear: first, we looked for the toponyms of the study sites or their geographical coordinates through Google Earth, and we obtained images that allowed us to locate its spatial position on the world map; second, we consulted online resources, with the aim of assigning to each location its corresponding mountainous regions (Appendix C1); and third, if we still had any doubts, we docked the shapefiles ADMIN (Appendix A1; Made with Natural Earth 2018) and GMBA inventory (Appendix A1; Körner et al., 2017) with the images we had obtained with Google Earth

– with the aim of assigning to each problematic location some of the mountains (polygons) of this last layer. For this process, we used the "Georeferencing" tool from QGIS 3.16.4. Hannover (QGIS Development Team, 2021).

2.1.2.2. Attribute reclassification and data standardization

Once the processes of reviewing and gathering information was completed, we proceeded to standardize the data obtained (Table B2).

For scientific names and their associated taxonomy, we consulted the GBIF database (Global Biodiversity Information Facility; www.gbif.org). For data of origin or native distribution range, we consulted CABI (Centre for Agricultural Bioscience International; www.cabi.org/isc/), the EOL (Encyclopedia of Life, eol.org), Plants of the World Online (http://www.plantsoftheworldonline.org/), and the USDA (United States Department of Agriculture; www.usda.gov) databases.

The native distribution ranges of the inventoried IASs were highly variable, both in extent and shape. Therefore, we classified the species according to their origin into six broad categories, based on the ecoregions or biogeographic realms of Olson et al. (2001): *Afrotropical*, *Australasian*, *Holarctic*, *Nearctic*, *Neotropical,* and *Palearctic*. We grouped the IASs that were native to the Indo-Malayan ecozone into the *Palearctic* category, as none of them were exclusive to the eastern region. For the same reason, we unified the kingdoms Australasia and Oceania into a single class (*Australasian*). As a special case, we added the *Holarctic* category, which included IASs with native distributions that extended to both the Nearctic and Palearctic. No IAS was native to Antarctica, so we excluded this category.

Finally, we classified the terrestrial habitats of the inventory into 11 broad categories, corresponding to the aggregate land use classes of GLC-SHARE 2014 (Latham et al., 2014): *artificial surfaces* (01), *croplands* (02), *grasslands* (03), *tree covered areas* (04), *shrubs covered areas* (05)*, herbaceous vegetation, aquatic or regularly flooded* (06), *mangroves* (07), *sparse vegetation* (08), *bare soils* (09), *snow and glaciers* (10) and *water bodies* (11).

2.1.2.3. Estimation of impact weights ($w_{i,j}$)

As shown below (section *2.2. Impact mapping*), the calculation of CIMPAL scores requires prior estimation of the impact weights ($w_{i,j}$), and there are two approaches to calculating them (Katsanevakis et al., 2016): the uncertainty-averse approach (Yemshanov et al., 2013) and the precautionary approach (Ojaveer et al., 2015). Each option represents a different decision-making strategy within the framework of management and conservation, and it is recommended to apply one or the other according to the objectives of each study (Katsanevakis et al., 2016). In our case, we used the uncertainty-averse approach; hence, we estimated the impact weights by combining two factors: the magnitude of the reported ecological impact and the strength level of their evidence (Figure D1 and Table D1). We chose this approach because the inventoried publications presented very different working methodologies, and therefore the consistency of their results was highly variable between studies.

We classified the publications into six categories, based on the type of study that had been conducted: manipulative experiments, natural experiments, modelling, direct observations, non-experimental correlations, and expert judgment (Table D2). From this information, we assigned each impact a strength level of its evidence: robust, medium, or limited (Table D1). In parallel, we classified the impacts according to their magnitude; thus, we used five semi-quantitative classes defined by Katsanevakis et al. (2014; 2016), which were based on the framework of Blackburn et al. (2014). Given the effect of each IAS on each habitat, we considered that the associated impacts could be minimal, minor, moderate, major, or massive (Table D1). At this point, we assigned a value to each impact weight ($w_{i,j}$): 0, 1, 2, 4, or 8 (Figure D1). In this way, we reduced the impact weights borne by weak evidence, compared to those that were well documented.

2.1.3. Occurrence data

2.1.3.1. IASs inventory subset

As a result of data extraction and the processes of complementation, standardization, and reclassification, we obtained an inventory of IASs (animals and plants) present in the world's mountain systems; these, in addition, were associated with at least one documented impact in the scientific literature (Table B2 and Table B3). The resulting inventory consisted of 130 species (51 animals and 79 plants), 106 genera, 52 families and 10 different classes, which together generated reported impacts on 6 continents: Africa, Asia, Australia, Europe, North America, and South America. To make the cumulative impact maps, we only selected those IASs with associated values Σw_i > 0 – as we considered they were the only ones that represented high impacts. Thus, finally kept a subset of 99 species (Table B3): 10 present in Africa, 18 in Asia, 3 in Australia, 17 in Europe, 53 in North America, and 11 in South America. Some IASs were documented in more than one continent.

2.1.3.2. Obtaining GBIF occurrence data

The occurrence records of the selected IASs were obtained through the GBIF database (www.gbif.org/es/occurrence/search). When searching for the data, we considered the GMRs impacted by each species (see the additional link cited in Table B3), and only downloaded the corresponding C-GMRs records for each case (Table A2). For those IASs with documented impact exclusive to one GMR (e.g., Rocky Mountains), we only obtained records from its corresponding C-GMRs (e.g., Canada, Mexico, and USA). However, for those that were present in more than one GMR (e.g., in the Appalachian Mountains and the Iberian Peninsula Mountain Ranges), we downloaded the data corresponding to all required C-GMRs (e.g., Canada, USA, Andorra, France, Portugal and Spain).

Of all the options offered by the GBIF search engine, we only selected the records that included the geographical coordinates, and we limited the search so that it only showed us occurrence points based on "observation", "machine observation", "human observation" or "literature". We excluded "material samples", "preserved specimens", "fossil specimens", "living specimens" and "unknown records". To convert GBIF geospatial data (CSV documents) to occurrence points in ESRI Shapefile format, we followed the procedure explained in Appendix A5.

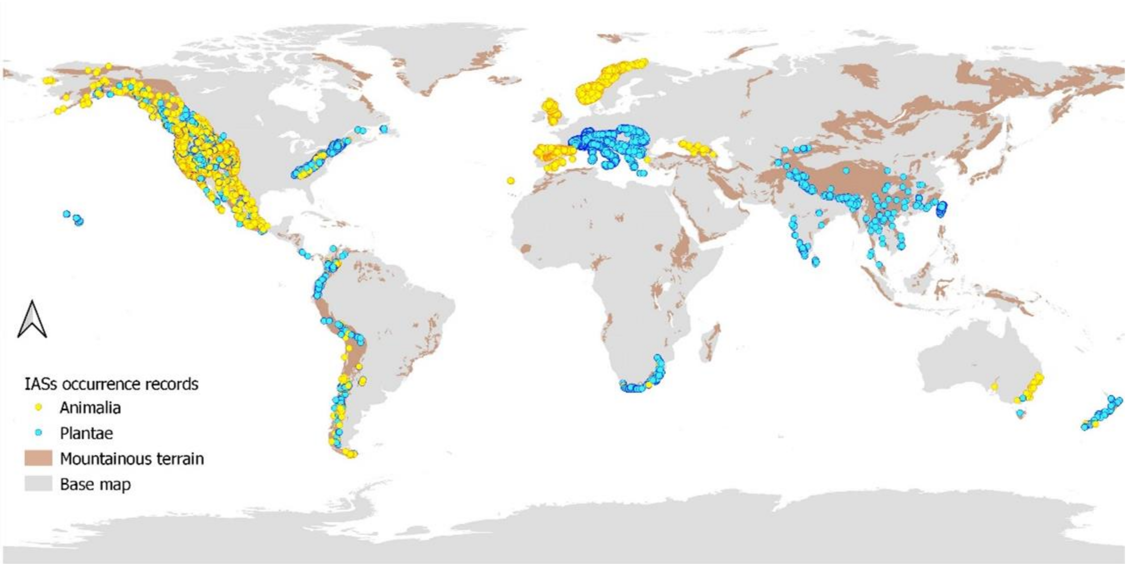
2.1.3.3. Occurrence records: exclusion and treatment

From the list of 99 IASs, we excluded 9 species because the GBIF database did not have occurrence records in the C-GMRs we had selected (Table B3). Through visual assessment, we also excluded *Herpestes javanicus* (documented as invasive in Japan, Asia) – as its occurrence records did not fall within the mountainous regions of the Japanese Ranges GMR.

Based on this subset of data (89 IASs), we selected which records were valid for mapping the cumulative impacts. For this reason, we referred to the IUCN (2020) definition of exotic species, according to which we could consider as such "*any species, subspecies or lower taxon that occurs outside its natural area, past or present"*. Thus, we consulted the origins of each species (Table B2) and proceeded as follows: first, we classified the species into two broad groups (Table B3), depending on whether they were non-native (group A) or native (group B) of the continent where the associated impact occurred; and second, we distinguished the records of the species of group B, considering their range of natural distribution. Out of the 89 species listed, 63 were in group A, 23 were in group B and 3 were in both groups (Appendix E). First, we filtered all the occurrence records downloaded from GBIF, to keep only those that were located within the polygons of the different GMRs. We performed this procedure using the QGIS geoprocessing tool "Intersect" (Appendix A6). By this first filtering process, we excluded 3 species: 2 from group A (*Festuca pratensis* and *Rhaponticum repens*; with reported impact in the Appalachian Mountains and Rocky Mountains, respectively), and 1 in group B (*Utricularia inflata*; Appalachian Mountains); none of the records of these species intercepted with the polygons of the layer GMBA inventory (Körner et al., 2017). We also excluded the impact of *Enterion tyrtaeum* (or *Octolasion tyrtaeum*) in the Appalachian Mountains, as we did not have occurrence data in this mountainous region; instead, we included it for mapping the Rocky Mountains, as it was listed as a documented invader in both GMRs. For group A species, we accepted all filtered occurrence points as valid; while for each of the species of group B: (a) we eliminated the points that intercepted with their natural distribution areas, and (b) we maintained those that were present in the introduced, non-native or not-indicated-as-natural zones.

We also excluded the records considered to be invalid (from group B) using information contained in the same articles or in additional literature (Appendix C2 and Table E1). For each problematic species, we looked for updated distribution maps indicating their native and introduced areas; in general, we obtained this information through: (1) specialized literature, which we found with Google Scholar by searching for the terms *Native distribution range* and the scientific name of the IAS; (2) official databases, such as those of the USGS (United States Geological Survey; www.usgs.gov), and (3) other online resources (especially from hunting or fishing websites). We downloaded all these files, and georeferenced them one by one using the QGIS "Georeferencing" tool. Then, we overlaid the vectorial occurrence points of the IASs corresponding to each of these maps and removed the points that fell within the natural areas of distribution (Appendix A7). As a result of this procedure, we excluded 2 species, eliminated occurrence points in 10 cases, and kept the data unchanged in 13 cases (Table E1). Among the IASs with deleted records, 7 were from Nearctic region, 4 from Palearctic and 2 from Holarctic. Finally, we combined all the final points layers (both group A and group B) and created a single layer that contained all the occurrence records we were interested in (Figure 1 and Appendix A8).

Figure 1. All the IASs' occurrence records used for cumulative impact mapping.



2.2. Impact mapping

2.2.1. Application of the adapted Katsanevakis model and impact mapping

Using the IASs inventory, we constituted the impact matrices (henceforth, AHWG matrices) which allowed us to assign impact weights ($w_{i,j,k}$) for each species *i*, habitat *j* and GMR *k* (Table B4). GMR factor was especially important because some IASs of the inventory were listed as present in more than one GMR with different $w_{i,j}$ values. To calculate CIMPAL scores we adapted the conservative additive model of Katsanevakis et al. (2016). First, we divided the total study area (GMBA polygons layer) using the GRID layer; and second, we estimated the CIMPAL scores for each of the cells, using the following formula:

$$I_{c,k} = \sum_{i=1}^{n} \sum_{j=1}^{m} A_i H_j w_{i,j,k}$$

Where *n* is the number of IASs; *m* is the number of habitats; *i* and *j* identify, respectively, each IAS and each habitat; A_i is the population status index of the species *i*, transformed and normalized in a range between 0 and 1; H_j is the extent of habitat *j*, also standardized in a range between 0 and 1, and $w_{i,j,k}$ is the impact weight associated with species *i*, habitat *j* and GMR *k.* We defined the parameter A_i as a binomial state variable, considering A_i = 1 in case of presence and A_i = 0 in case of absence or no-data. In addition, (1) we considered that impact weights were spatially constant along the same GMR; and (2) for each IAS *i* and GMR *k*, we calculated the impact weights according to the highest impact reported in each GMR – which is a precautionary simplification on the spatial variability of the impact.

Given that grid cells did not have the same size across the study area (with differences within and between GMRs, depending on latitude), we standardized the cumulative impact values (hereinafter, StCIMPAL scores) by the cell area (in km²) – using the QGIS "$area" function of the "Field calculator" tool.

We applied this methodology using the R packages *dplyr* (*v1.0.7.*; Wickham et al., 2021) and *sf* (Pebesma, 2018) on RStudio 1.3.1093 (R Core Team, 2021). The full reproducible code is available in Appendix A4. We conducted some spatial steps and drawn the impact maps using QGIS 3.16.4. Hannover (QGIS Development Team, 2021). We classified StCIMPAL scores using Natural Breaks (Jenks) to better identify impacted areas.

We estimated the indicators D_2, D_3 and D_4 of Katsanevakis et al. (2016) to compare the relative importance of each IAS in the cumulative impacts. For each IAS we calculated: (D_2) the number of cells with impact > 0 and presence of the species*;* (D_3) the sum of its impact values (not CIMPAL scores), and (D_4) its average impact value, considering the whole occurrence area (estimated through the number of cells with the presence of that species). Indicators D_2 and D_3 provide information on each species in terms of impact on a global scale, and indicator D4 expresses the magnitude of the impact on the invaded localities – and therefore allows for a local-scale analysis (Katsanevakis et al., 2016). We also estimated the maximum potential impact on each habitat as the sum of all impact weights of all IASs for this habitat (i.e., $\Sigma_i w_{i,j}$).

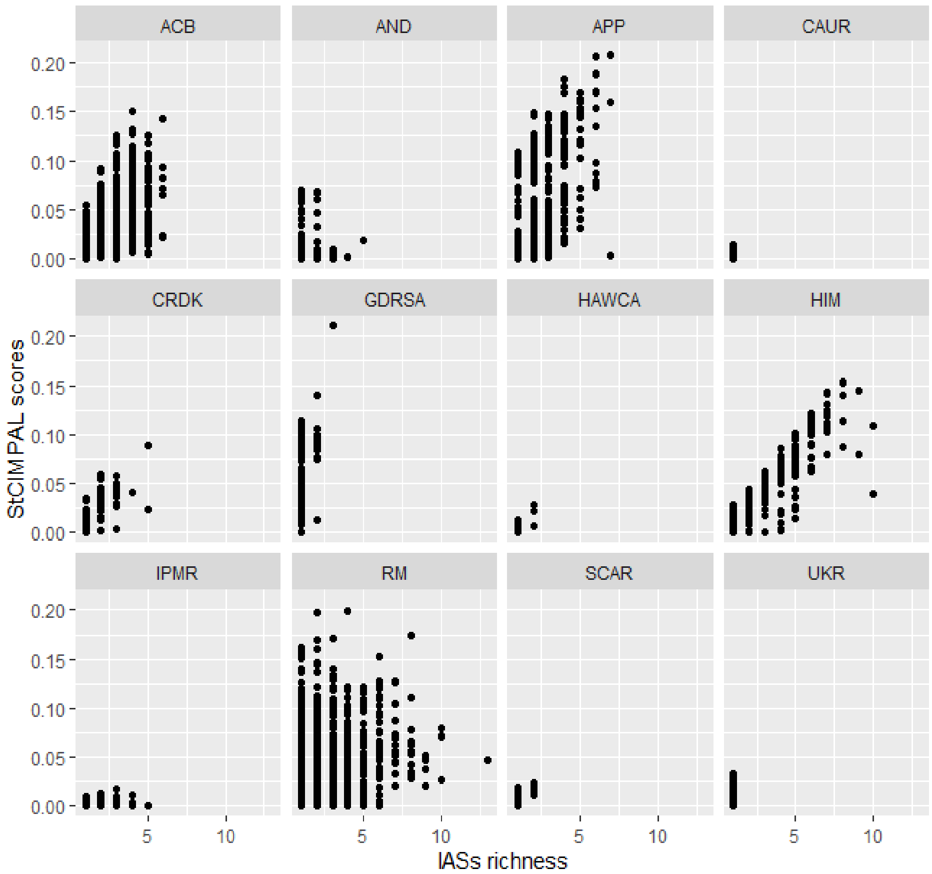
2.3. Data analysis

Our dataset consisted of non-repeated cells records with unique values of StCIMPAL scores, IASs richness, average elevation, and biogeographic information. We compiled the impact maps from this global dataset (14487 rows) but performed the statistical analysis through a subset of data (hereinafter, SST1; 12918 rows), obtained after eliminating rows with useless elevations – i.e., nulls (in margin cells), and negatives values (e.g., in coastal mountains near deep marine areas).

Then, we carried out data exploration following the protocol described in Zuur et al. (2010). The response variable (StCIMPAL scores) had a low zero ratio (≈ 23%) but remained zero-inflated and over-dispersed: its distribution had a probability mass at the origin, accompanied by a skewed continuous distribution over the positive values. We investigated StCIMPAL scores by GMR and found that, in general, they all had that shape. Despite this, CAUR and UKR StCIMPAL values had more regular distributions. We then delved into IASs richness and decided to create a second dataset (SST2, 12475 rows and ≈24% of zero-values) excluding both CAUR and UKR data from SST1 due to lack of variability (Figure 2). We conducted all statistical analyses using RStudio 1.3.1093 (R Core Team, 2021). We set significance level as $P < 0.05$ for all tests, with $0.05 < P < 0.1$ deemed as a trend. We performed all tests two-tailed and transformed data as necessary to meet model assumptions.

As complementary analyses, we conducted a Kruskal-Wallis Test on STS1 to find significant differences in StCIMPAL scores among GMRs. We then applied pairwise comparisons using Wilcoxon rank sum test with continuity correction (*P*-value adjustment method: Bonferroni) to compare these measures between each pair of GMRs. We used functions from R packages *agricolae* (*v1.3-5;* de Mendiburu, 2020), *biostat* (*v1.0.2*; Gegzna, 2020), *rstatix* (*v0.7.*0; Kassambara, 2021) and *tidyverse* (Wickham et al., 2019).

Figure 2. Relation between IASs richness and StCIMPAL scores by GMR, showing the lack of variability of CAUR and UKR.



We then estimated the effect of average elevation (continuous variable), IASs richness (discrete) and GMRs (categorical, with twelve levels) on StCIMPAL scores by fitting three Tweedie's compound Gamma-Poisson generalized linear models (CPGLMs) with a log link function (to ensure positive fitted values). We considered the partial effects of all three main terms and the relevant interactions between them. We removed the three-way interaction ($GMR \times Elevation \times IASsRichness$) to facilitate the results interpretation.

$$NStCIMPAL_i \sim Tweedie(\mu_i, \varphi_i, p)$$

$$E(NStCIMPAL_i) \sim \mu_i$$

$$Var(NStCIMPAL_i) \sim \varphi \cdot {\mu_i}^p$$

$$\varphi > 0$$

$$p \in (1,2)$$

$$\log(\mu_i) = GMR + Elevation$$ **Equation (1)**

$$\log(\mu_i) = GMR + IASsRichness$$ **Equation (2)**

$$\log(\mu_i) = GMR + Elevation + IASsRichness + GMR \times Elevation + GMR \times IASsRichness + Elevation \times IASsRichness$$ **Equation (3)**

In all cases, we verified model assumptions, plotting residuals versus fitted values and versus each covariate in the models. To fit the models in the equations, we used SST1 dataset and the function *cpglm* from R package *cplm* (Zhang, 2013). As complementary analyses, we repeated all three models by applying a square root transformation to the StCIMPAL scores – which allowed for better fitted residuals. Then, we obtained the estimated marginal means by re-fitting the non-transformed final models as new Tweedie GLMs, using functions *glm* (R package *stats, v3.6.2;* R Core Team, 2021) and *tweedie* (*statmod*, *v1.4.36;* Giner and Smyth, 2016), since other options presented incompatibility. We applied post hoc Tukey multiple comparisons among GMRs (through Model 1 – fitted with Equation 1; *P*-value adjustment method: Bonferroni), using function *emmeans* (*lsmeans*; Lenth, 2016).

3. RESULTS

3.1. StCIMPAL values: estimation and mapping

CIMPAL and StCIMPAL scores showed strong spatial heterogeneity and ranged from 0 to 16.93 and from 0 to 0.21, respectively. Impacted cells appeared to be aggregated, and some impacted hotspots could be differentiated (Figure 3 and Figure F1), especially in the Alps (ACB), the French Massif Central (ACB), the Appalachian Mountains (APP), the Rocky Mountains (RM), Taiwan (HIM), the Cape Ranges (CRDK), the Great Dividing Range (GDRSA) and the Southern Alps (GDRSA). Some heavily impacted areas partially coincided with IASs-rich zones (Figure F2). Despite this, we found impacted cells scattered throughout all the study area.

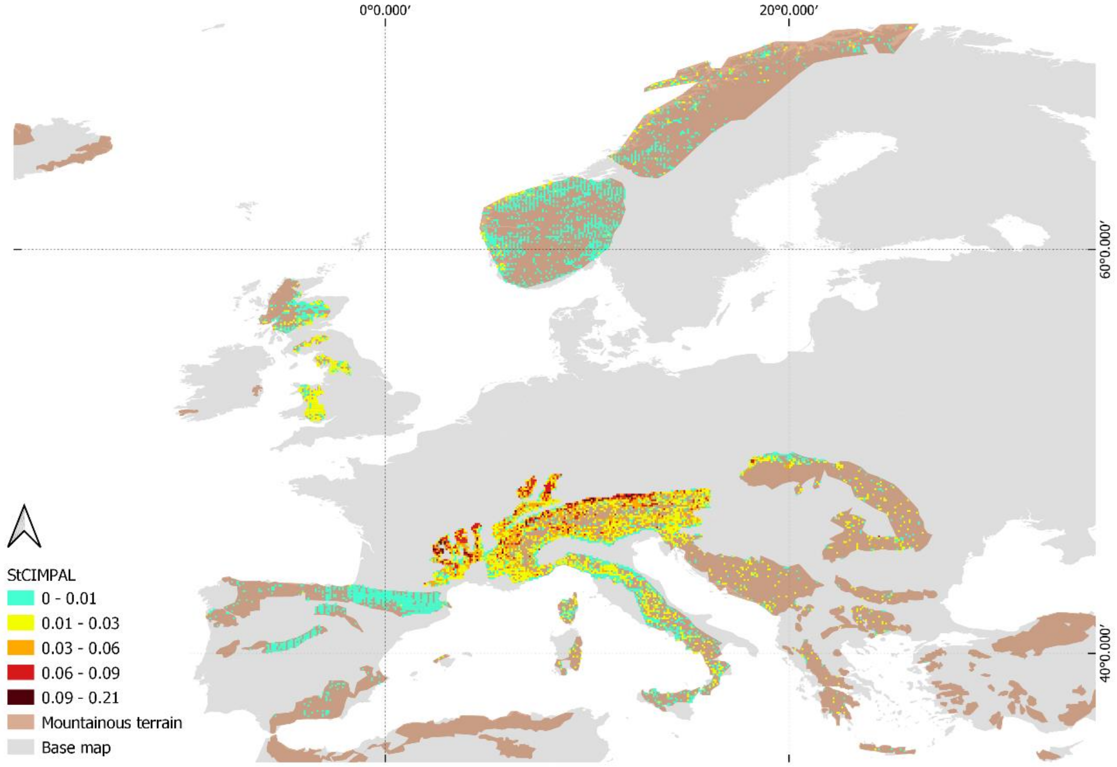
3.2. Elevation and IASs richness

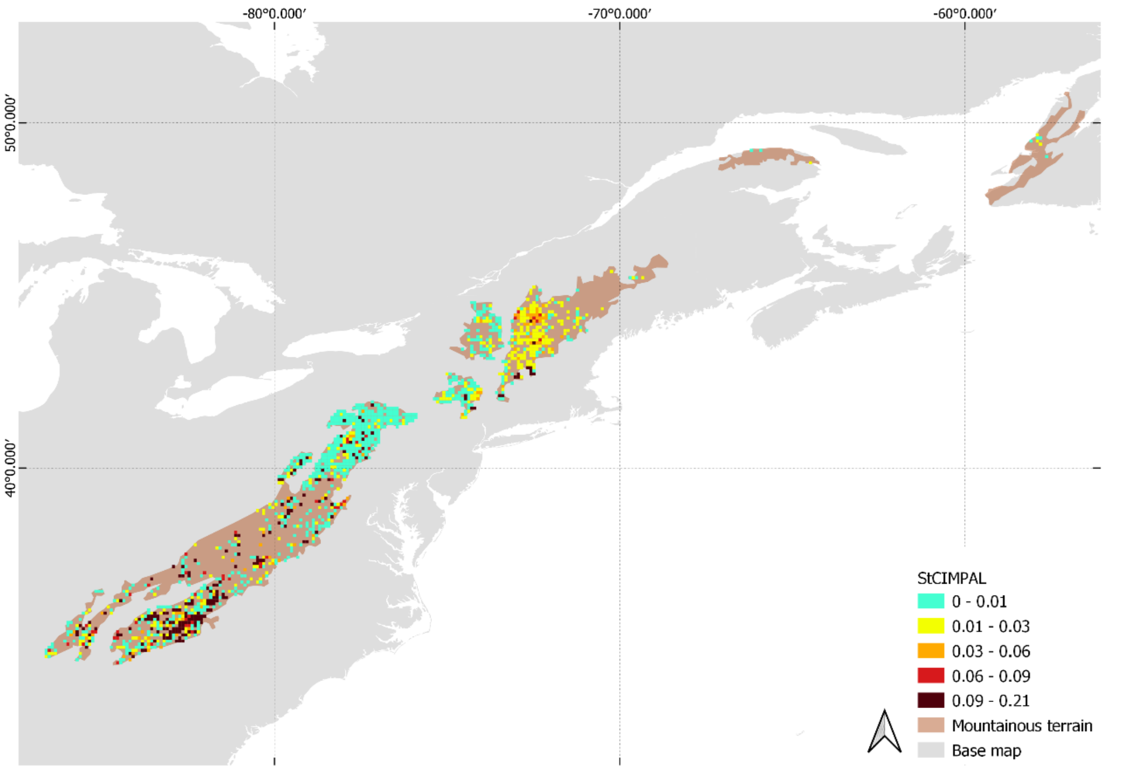
The maximum mean elevation values of truly impacted cells (with a StCIMPAL score > 0; hereinafter, TIC) were different among GMRs. AND (4877 meters ASL), HIM (4724) and RM (4267) were the GMRs with impact at higher altitudes, followed by CAUR (3444) and ACB (3205). IPMR (2392) presented maximum values at moderate altitudes, while at GDRSA (1804), SCAR (1720), CRDK (1524), HAWCA (1500), APP (1427) and UKR (890) they were at low altitudes.

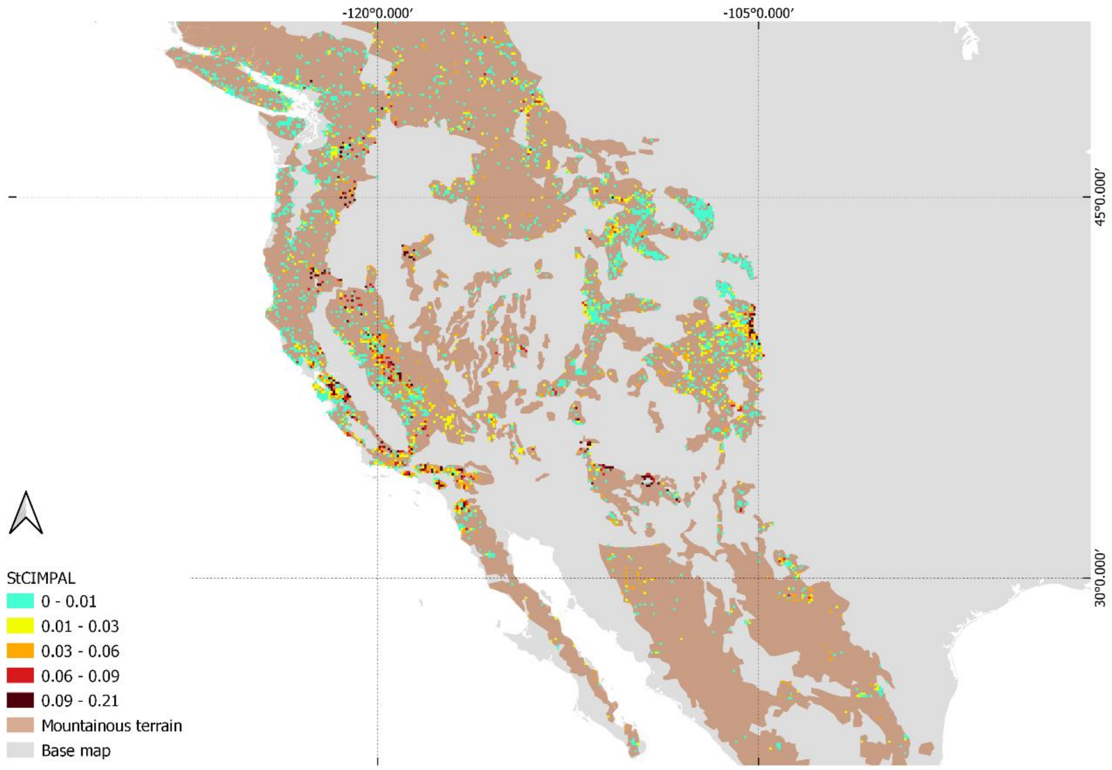
RM (13 IASs species) and HIM (10) were the GMRs with the maximum values of IASs richness per cell, followed by APP (7), ACB (6), AND (5), CRDK (5), IPMR (5), GDRSA (3), HAWCA (2) and SCAR (2). Only CAUR and UKR had 1 IAS as a maximum value. Those results were equal both considering all cells and only TIC, except for IPMR – with 4 IASs as a maximum value in this second case.

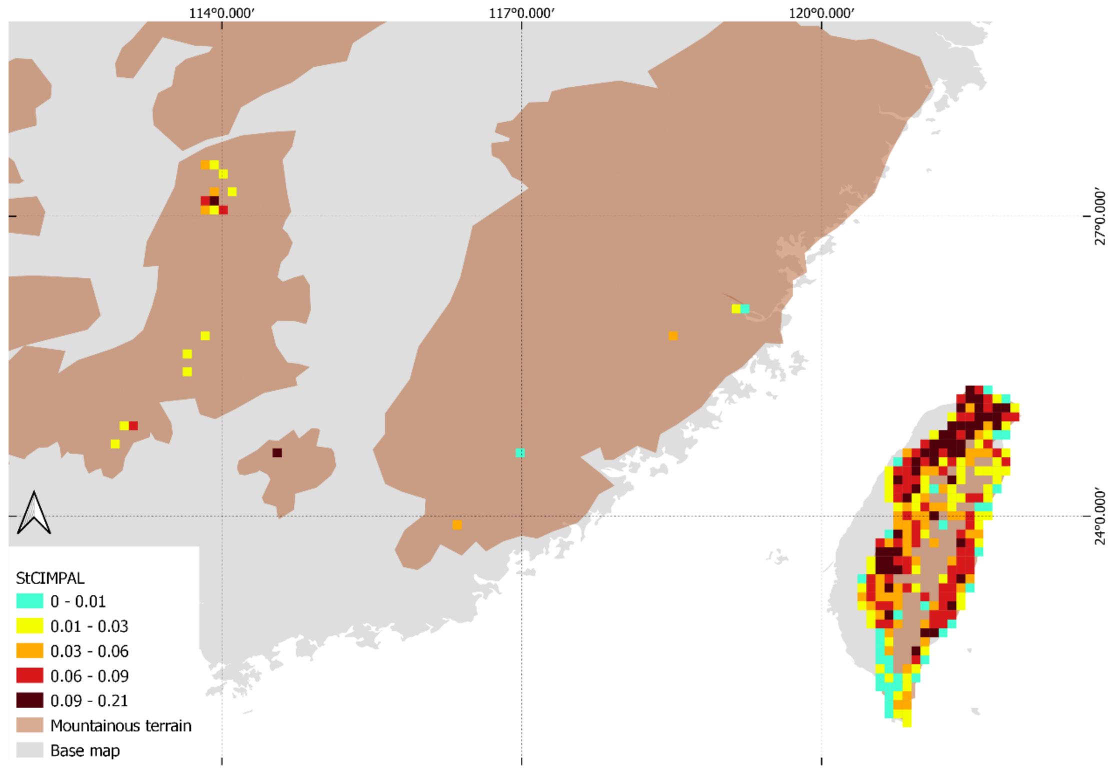
The maximum IAS richness values per TIC were in different elevations in each GMR. Despite this, they followed similar patterns: in RM, these values were near sea level (NSL, < 500 meters ASL); in GDRSA, at low elevations (500-2000); in ACB, APP, CRDK, HAWCA, HIM, SCAR, and UKR, they ranged from NSL to low elevations; and in AND and IPMR, they were at moderate elevations (2000-3000). CAUR showed 1 IAS as the maximum value, which ranged between NSL and high elevations (> 3000 m ASL).

Figure 3. Maps of the mountainous regions of the world with the largest number of impacted cells: A) Europe; B) APP, USA, North America; C) RM, USA, North America; D) Taiwan, HIM, China, Asia. The most affected areas are represented in red shades. The cyan cells represent areas with IASs presence but without impact or low impact values. Extensions without impact cells represent the areas without IASs occurrence points. Although it does not appear on the map, the northern and southern regions of the RM also showed a high density of impacted cells.





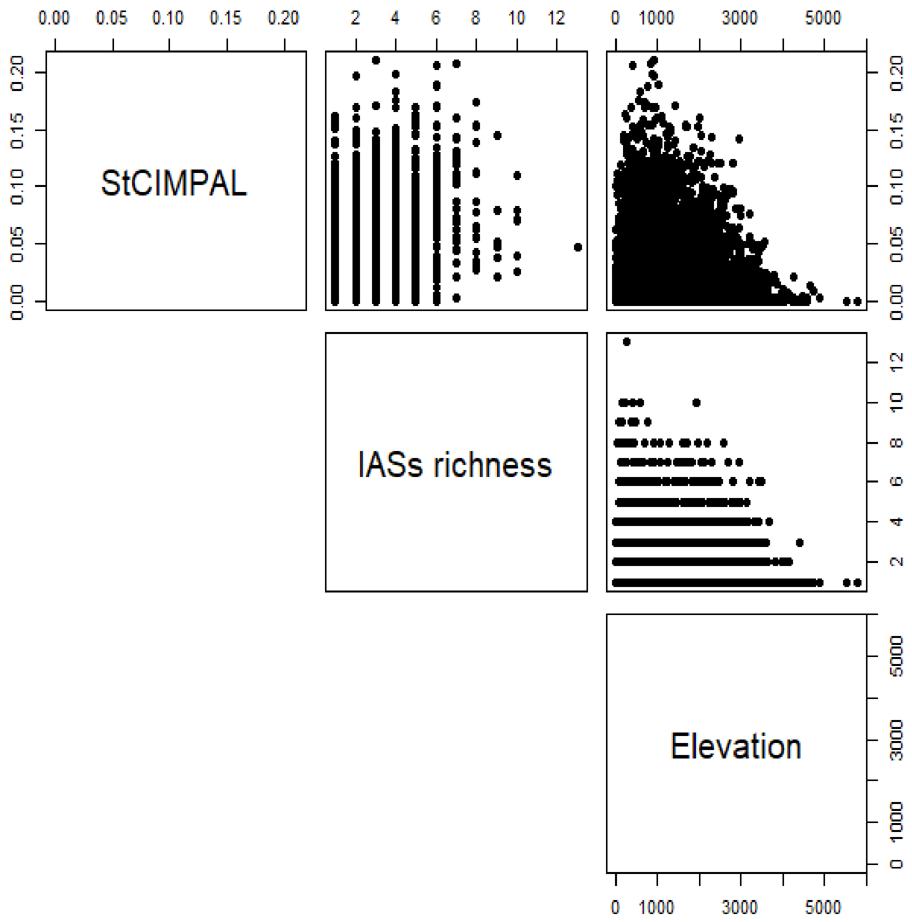




3.3. Testing the effects of GMRs, elevation and IASs richness on StCIMPAL scores

We found clear patterns between StCIMPAL scores and both elevation and IASs richness (Figure 4). However, the GMRs appeared to have particular relationships between the cumulative impact values and both covariates, especially for elevation. We plotted the response variable with relative to the covariates and we found that ACB, APP, CRDK, HIM, and RM showed similar positive correlations between StCIMPAL scores and IAS richness (Figure 2), both using raw and square root transformed impact values; in the case of elevation, the relationship was more heterogeneous, and only ACB, HIM, and RM appeared to have truly similar patterns (Figure F3). We tested collinearity between elevation and IASs richness for both STS1 and STS2, and we found no significant linear relationships in both cases. Models' validation indicated no problems. StCIMPAL scores differed by GMR in all three models (Model 1, Model 2, and Model 3; Table 1, Table F1 and Table F2, respectively). We also obtained similar results in square root transformed models (Model 4, Model 5, and Model 6; Table F3, Table F4 and Table F5, respectively).

Figure 4. Relationships between StCIMPAL scores, IASs richness and elevation (in meters) using SPS1 dataset. Lowest values in IASs richness plots are 1, not 0.



In Models 1, we found significant effects of elevation (T_{12894} = 9.202, $P < 2e^{-16}$) on StCIMPAL scores, as well as significant interactions with the categorical variable GMR (Table 1). HAWCA and UKR showed non-significant effects on StCIMPAL scores (T_{12894} = -0.516 and 0.958, P = 0.606 and 0.338, respectively), while CAUR only showed a trend (T_{12894} = -1.902, P = 0.057). It should be noted, however, that the interaction between elevation and HAWCA ($T_{12894)}$ = -2.038, P = 0.042) and UKR (T_{12894} = -4.151, P = 3e-05) did prove to be significant. We also found non-significant interaction between elevation and IPMR (T_{12894} = 0.023, P = 0.982), but CAUR and GDRSA showed trendy interactions (T_{12894} = -1.737 and -1.803, P = 0.082 and 0.071).

Table 1. Model 1. Estimated regression parameters, standard errors, t values, and *P*-values for the Tweedie's compound Gamma-Poisson GLM presented in Equation (1). The estimated value for φ and p were 0.202 and 1.537 respectively. Model AIC: -42109. Degrees of freedom: 12894. We used SPS1 dataset.

	Estimate	Std. Error	t value	P-value	
Intercept	-3.824	0.0323	-118.631	<2e-16	***
GMRAND	0.512	0.162	-3.160	0.002	**
GMRAPP	-0.437	0.078	-5.602	2e-08	***
GMRCAUR	-0.837	0.440	-1.902	0.057	.
GMRCRDK	0.650	0.221	2.946	0.003	**
GMRGDRSA	1.071	0.125	8.563	<2e-16	***
GMRHAWCA	-0.306	0.592	-0.516	0.606	
GMRHIM	0.696	0.084	8.277	<2e-16	***
GMRIPMR	-4.465	0.248	-18.027	<2e-16	***
GMRRM	0.166	0.049	3.415	6e-04	***
GMRSCAR	-1.513	0.111	-13.693	<2e-16	***
GMRUKR	0.138	0.145	0.958	0.338	
Elevation	3e-04	3e-05	9.202	<2e-16	***
GMRAND : Elevation	-9e-04	7e-05	-11.650	<2e-16	***
GMRAPP : Elevation	0.001	1e-04	8.450	<2e-16	***
GMRCAUR : Elevation	-5e-04	-3e-04	-1.737	0.082	.
GMRCRDK : Elevation	-0.002	3e-04	-7.373	2e-13	***
GMRGDRSA : Elevation	4e-04	2e-04	-1.803	0.071	.
GMRHAWCA : Elevation	0.001	7e-04	-2.038	0.042	*
GMRHIM : Elevation	-4e-04	6e-05	-7.020	2e-12	***
GMRIPMR : Elevation	-5e-06	2e-04	0.023	0.982	
GMRRM : Elevation	-4e-04	-4e-05	-11.501	<2e-16	***
GMRSCAR : Elevation	-0.002	2e-04	-10.472	<2e-16	***
GMRUKR : Elevation	-0.002	4e-04	-4.151	3e-05	***

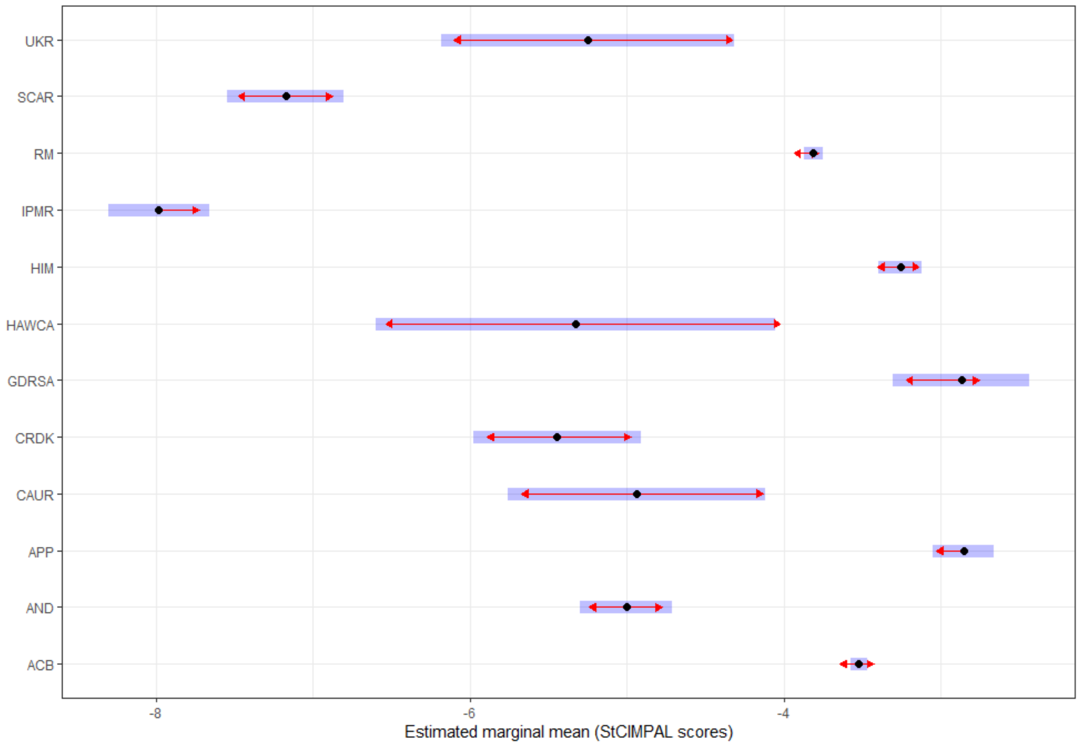
In Model 2, we found significant effects of IASs richness on StCIMPAL scores (T_{12429} = 30.578, P < 2e^{-16}), as well as significant interactions with GMRs (Table F1). HIM showed non-significant effects on StCIMPAL scores (T_{12429} = -0.609, P = 0.542), while its interaction with IASs richness was significant (T_{12429} = -2.191, P = 0.029). We found that interactions between IASs richness and AND (T_{12429} = 0.323, P = 0.747), GDRSA (T_{12429} = 0.424, P = 0.671), HAWCA (T_{12429} = 0.234, P = 0.234) and IPMR (T_{12429} = 1.186*,* P = 0.236) were non-significant.

In Model 3, we found significant effects of elevation (T_{12418} = 7.227, P = 5e^{-13}) and IASs richness (T_{12418} = 25.340, P < 2e^{-16}) on StCIMPAL scores, as well as significant interactions with GMRs (Table F2). We also found a significant interaction between elevation and IASs richness (T_{12418} = 4.373, P = 1e^{-05}). AND, CRDK and HAWCA showed non-significant effects on StCIMPAL scores (T_{12418} = -1.477, -0.047 and -0.889, P = 0.140, 0.963 and 0.374, respectively). We found trends between elevation and HAWCA (T_{12418} = -1.842, P = 0.066) and IPMR (T_{12418} = -1.748, P = 0.08), and between IASs richness and AND (T_{12418} = 1.762, P = 0.078). However, the interactions between IASs richness and GDRSA (T_{12418} = 0.473, P = 0.636), HAWCA (T_{12418} = 1.026, P = 0.305) and IPMR (T_{12418} = 0.987, P = 0.324) were non-significant.

Post hoc comparisons in Model 1 showed significant differences among GMRs. We found that: (a) AND did not differ from CAUR (Z = -0.217, P = 1.0), CRDK (Z = 2.072, P = 0.643), HAWCA (Z = 0.709, P = 1.0) and UKR (Z = 0.723, P = 1.0); (b) APP did not differ from GDRSA (Z = 0.085, P = 1.0); (c) CAUR did not differ from CRDK (Z = 1.481, P = 0.946), HAWCA (Z = 0.737, P = 1.0) and UKR (Z = 0.722, P = 1.0); (e) CRDK did not differ from HAWCA (Z = -0.242, P = 1.0) and

UKR (Z = -0.515, *P* = 1.0); (f) GDRSA did not differ from HIM (Z = 2.458, *P* = 0.367), and (g) HAWCA did not differ from UKR (Z = -0.138, *P* = 1.0). The remaining multiple comparisons turned out to be significant. Finally, we identified the low-impacted GMRs (IPMR and SCAR), and the high-impacted ones (ACB, APP, GDRSA, HIM and RM) (Figure 6). These results matched the cumulative impact maps.

Figure 6. Plotted post hoc comparisons in Model 1. The blue bars are confidence intervals for the EMMs, and the red arrows are for the comparisons among them. If an arrow from one mean overlaps an arrow from another group, the difference is not significant (Lenth, 2016).

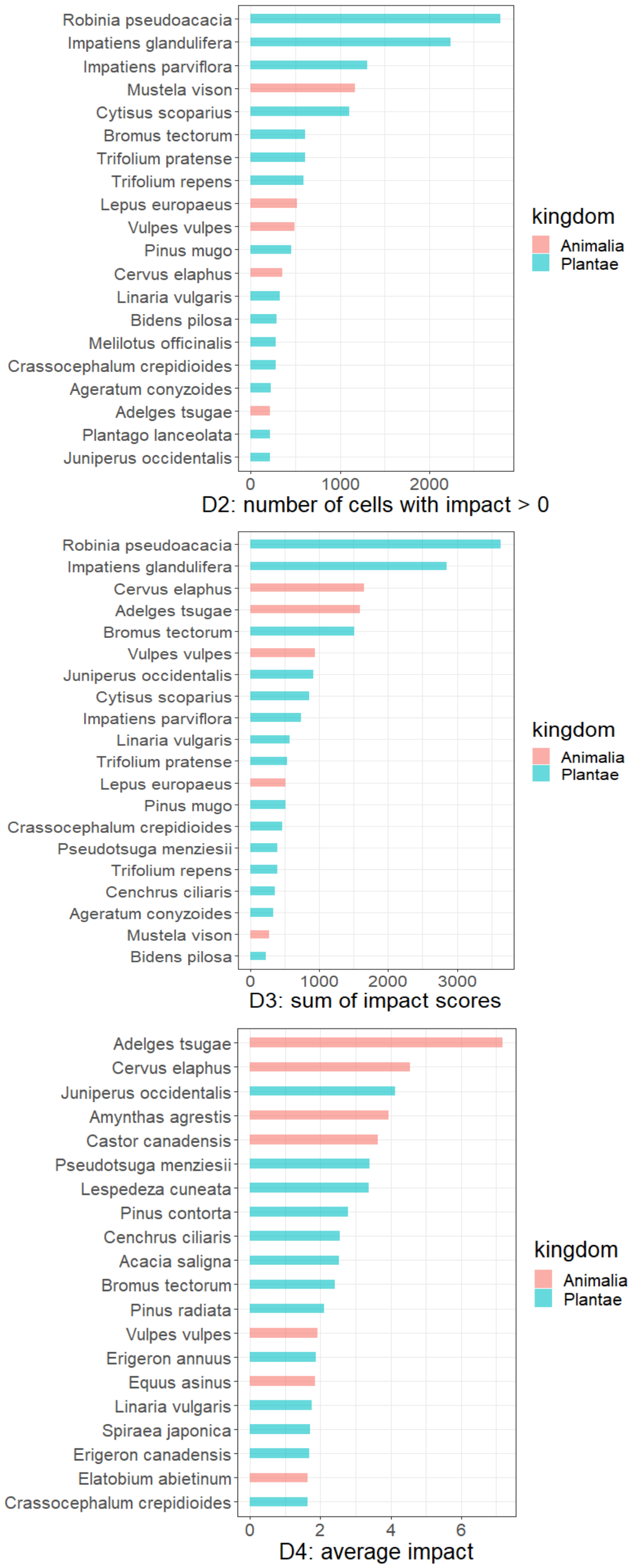


The complementary Kruskal-Wallis Test on STS1 also showed statistically significant differences in StCIMPAL scores between GMRs, $X^2(11, N=12918) = 3626.6$, $P < 2.2e^{-16}$, with a mean rank StCIMPAL score of 0.028 for ACB, 0.004 for AND, 0.029 for APP, 0.007 for CAUR, 0.012 for CRDK, 0.061 for GDRSA, 0.007 for HAWCA, 0.037 for HIM, 0.0003 for IPMR, 0.021 for RM, 0.002 for SCAR and 0.016 for UKR (Appendix F1 and Figure F4; Post hoc: Table F6).

3.4. Indicators

We estimated which IASs were the most problematic by creating rankings of the species with the highest associated impact (Figure 7). However, when quantifying the relative impacts, we obtained different results depending on the indicator used. D_2 allowed us to know which impacting IASs occupied the largest area in the world's map. The most common species were *Robinia pseudoacacia*, *Impatiens glandulifera* and *Impatiens parviflora* (all plants), followed by *Mustela vison* (animals) and *Cytisus scoparius* (plant) – in that order. Based on D_3, which also considers the severity and extent of the impacts, the ranking of the top-5 species was: *Robinia pseudoacacia* and *Impatiens glandulifera* (plants), *Cervus elaphus* and *Adelges tsugae* (Animals) and *Bromus tectorum* (plant). The five species with the highest local impact (estimated with D_4) were: *Adelges tsugae* and *Cervus elaphus* (animals), *Juniperus occidentalis* (plant) and *Amynthas agrestis* and *Castor canadensis* (animals).

Figure 7. Relative importance of the high-impact species as assessed by three indicators: D_2, D_3 and D_4. Only the top 20 species are shown in the charts.



3.5. Additional results: other effects on impact values

In Model 7, we found significant effects of the kingdoms (T_{23786} = 7.598, $P < 3e^{-14}$) on the impact values (Table F7); post-hoc analyses in this model also show that plants are linked to higher impact values (Z = -7.598, $P < 1e^{-04}$; Figure F5). Other taxonomic levels could explain part of the variability.

In Model 8, we found significant effects of the native ecozones on impact values (Table F8), except for the category *Australasian* (T_{23782} = 1.582, P = 0.114). We mapped impact values by native ecozones (Figure F6) and found that they are unevenly distributed along the earth's surface. Palearctic species were the most widespread IAS in the world. IASs from some regions of the world could be more problematic than others (Buckley and Catford, 2016; Rehmánek and Simberloff, 2017), but we should do additional analysis to verify this hypothesis.

Finally, we found that the habitats with the highest value of maximum potential impact at global scale (considering all 130 IASs) were tree covered areas (with $\Sigma_i w_{i,j}$ = 138), grasslands ($\Sigma_i w_{i,j}$ = 90) and water bodies ($\Sigma_i w_{i,j}$ = 82), followed by shrubs covered areas ($\Sigma_i w_{i,j}$ = 75) and sparse vegetation ($\Sigma_i w_{i,j}$ = 46). We need future work to expand this line of research.

4. DISCUSSION

Our results point to a global impact of IASs on mountains, with potentially profound effects on species, populations, and ecosystem processes (Mooney et al., 2005). We also evidence that the world's mountain systems exhibit variability in the graveness and distribution of impacts caused by IASs, and that these differences occur both within and among great mountain ranges. In this regard, we could enter a very complex discussion (Pauchard et al., 2009; Seipel, 2012, Seebens et al., 2017) but we will focus on basic and descriptive aspects of our work. We will develop new lines of interpretation in future revisions of this study.

Elevation and IASs richness have significant effects on the severity of cumulative impacts, and in addition, both variables explain part of the among-GMRs variability. We found that cumulative impact values decrease with increasing elevation and are positively correlated with IASs richness; moreover, IASs richness decreases as elevation increases, as has been seen in previous studies on oceanic islands and continental regions (Ullmann et al., 1995; Pauchard and Alaback, 2004; Daehler, 2005; Becker et al., 2005; Kalwij et al., 2008; Jakobs et al., 2010; Seipel et al., 2012; Barni et al., 2012; Otto et al., 2014; Siniscalco and Barni, 2018). Our results show that the altitudinal distribution of IASs richness varies among great mountain ranges and, therefore, there is no unique global pattern.

We would like to highlight some interesting exceptions. The Appalachian Mountains show a positive trend between the cumulative impact scores and elevations, and the Great Dividing Ranges and Southern Alps are clear examples of some areas with very high impact values, despite having few IASs. In the first case, the reason is not obvious, but we suggest that lowlands and highlands in Appalachian Mountain could present very marked distinctive features. This issue, however, should be investigated in depth. In the second case, we found that species that cause local impact on GDRSA are related to a reported high impact and are present at high densities – so the results obtained are logical and coherent. These facts reaffirm the validity of the methodology created by Katsanevakis et al. (2016), as the severity of impacts may depend, beyond the richness of invasive alien species, on intrinsic factors of the IASs and/or the ecological characteristics of the impacted habitats. To check the real effect of elevation on impact values, it would be advisable to monitor the presence of disturbed habitats, the conservation policies, and the control measures applied in these regions, as they could act as confounding factors.

Both animals and plants have a high impact on mountain ecosystems, and the species *Adelges tsugae*, *Cervus elaphus*, *Impatiens glandulifera* and *Robinia pseudoacacia* are some of the most problematic – at least, in this assessment. To interpret these results, we will use Plantae as a case study – as it is the kingdom with the highest associated impact, and at the same time, it is the most studied by other authors:

In general, the distribution of non-native plants varies along gradients of elevation and human disturbance, and their interactions are influenced by abiotic and biotic processes that interact on a wide range of spatial scales (Seipel et al., 2012). On the one hand, within the main ecological factors, we can distinguish four basic conductors that modulate invasions in mountain habitats; these are: 1) pre-adaptation of non-native species to abiotic conditions, 2) natural and anthropogenic local disturbances, 3) biotic resistance of established communities, and 4) propagule pressure (Kühn and Klotz, 2008; Pauchard et al. 2009; Ricciardi, 2013; Spear et al., 2013; Siniscalco and Barni, 2018). Within the geographical factors, the elevation and IASs richness are possibly among the most studied (Seipel et al., 2012): elevation is an intrinsic factor of mountain systems and, therefore, is considered easily controllable and interpretable (Alexander et al., 2009); while the IASs richness, in contrast, can be influenced by many components of the system – which can be intrinsic, such as global species richness, and extrinsic, such as its link to international trade (Westphal et al., 2008). Most of the problematic plants considered in our work meet most of the profitable characteristics in mountain environments and are found in localities with favourable abiotic conditions – that allow them to unleash their full invasive potential, and subsequently, their full impact potential.

Keeping in mind the framework of global change and the fact that invasions facilitate new invasion processes, it is likely that the current impacted areas would shift in a near future; many IASs could occupy larger areas and higher altitudes, but these changes are likely to occur unevenly among mountainous biogeographic regions (Chornesky et al., 2003; Abramova, 2012; Lee & Lee, 2006). Lowlands with projections to present greater IASs richness could be the most affected areas, especially if they are in the Alps, the French Massif Central, the Appalachian Mountains, the Rocky Mountains, Taiwan, the Great Dividing Range, and the Southern Alps. In any case, they are known to have well-preserved natural habitats (Pauchard et al., 2009; Catalan et al., 2017), and therefore, we recommend optimizing existing elevational protections or creating new ones – in agreement with Elsen et al. (2018).

Although GBIF is considered a good tool for evaluating biodiversity studies, its data presents an inherent geographic and taxonomic bias (Beck et al., 2013; Maldonado et al., 2015; Shirey et al., 2019). This lack of data is especially evident in Africa, Asia, and South America (Pyšek et al., 2008). Areas without data cannot be evaluated so easily, and for this reason, we recommend promoting and implementing participatory monitoring measures, such as citizen science projects (Chandler et al., 2017).

In conclusion, despite being exhaustive, we cannot extract a balanced understanding of the overall effect of IASs on a global scale, as we may not be aware of specific invasions of poorly studied regions. In this regard, we consider our work as a rapid approximation of the spatial and altitudinal patterns that modulate the cumulative impacts of IASs on mountain ecosystems. However, we reveal that: 1) the relationship between cumulative impact scores and IASs richness in terrestrial mountain systems differs between biogeographic regions, and 2) local average elevation has an effect that also varies depending on the great mountain range where the impacts occur. Our approach constitutes a significant step towards informing IASs context, and has heuristic value for generating further hypothesis about IASs impacts and spread.

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Supplementary Materials and Data

APPENDICES

Mapping the impact of invasive alien species on mountain ecosystems

MSc Thesis

Master's degree in Terrestrial Ecology and Biodiversity Management

Terrestrial Ecology specialization

2020 – 2021

Department of Animal Biology, Vegetal Biology and Ecology

Faculty of Biosciences

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APPENDIX A – This appendix includes all the processes done with QGIS 3.16.4. Hannover (QGIS Development Team, 2021) and RStudio (R Core Team, 2021), explained step by step. We created several projects to perform all steps.

Appendix A1 – GMBA layer preparation and creation of GMR groups:

1. We loaded the vector layer *ne_10m_admin_0_countries* (Admin 0 – Countries, 1:10m V4.1.0; Made with Natural Earth 2018) and set the SRC to EPSG: 4326 – WGS 84. We used this layer as a base map (hereafter, we will refer to this layer as ADMIN).
2. We loaded the vector layer *GMBA Mountain Inventory_v1.2-World* (Körner et al., 2017), which showed the full world-wide inventory of mountains (formed by 1048 polygons). Its attribute table included only object name, country, and the online resource used for its identification (if available), so we added manually the *Continent* column; to do this, we clicked on "Open Attribute Table" and proceeded as follows: "Switch edit mode" > "New field" > "Name": *Continent*; "Type": Text (string); "Length": 15. In addition, we added an ID for each polygon via: "Field Calculator" > "Input Layer": *GMBA Mountain Inventory_v1.2-World* [EPSG: 4326]; "Field name": *ID_mountain*; "Result field type": Integer; "Result field length": 5; "Result field precision": 0; "Formula" > "Expression": $id. The resulting layer was *GMBA Mountain Inventory with ID*.
3. We modified the attributes of one polygon because it contained erroneous information – specifically, Futa Djalon polygon, which was listed as a mountainous region of Guyana, when it is part of Guinea.
4. We fixed the invalid polygons (e.g., poorly closed), through the steps outlined at the following tutorial: *https://www.qgistutorials.com/en/docs/3/handling_invalid_geometries.html*.
5. We grouped the polygons of the *GMBA Mountain Inventory with ID* layer into 20 different groups and obtained as a result 20 new vector layers (Table A1). We proceeded as follows: (1) we manually selected the polygons we were interested in grouping using "Select objects by area or a single click", (2) we right-clicked on the *GMBA Mountain Inventory with ID* layer > "Export" > "Save selected objects as" > "Save vector layer as" > "Format": ESRI shape file; "File name": [GMR name]; "SRC": EPSG: 4326 – WGS 84; "Encoding": UTF-8, and we selected the option "Save only selected space objects". We left the other options as they were by default. We added the *GMR* column to each GMR layer and assigned an identification code to each GMR (e.g., global resulting layer: *GMBA_MI_with_IDm_GMR*; we did the same for every GMR layer).

Although the GMBA Mountain Inventory was also available in 8 sets of GIS files (one for each mega-region of the world: Africa, Asia, Australia, Europe, Greenland, North America, Oceania, and South America), we decided to use the global layer – because it contained 3 more mountainous areas, corresponding to 4 polygons: Coro Region SA (1 polygon), Venezuelan Coastal Range SA (2), and Nuba Mountains AF (1).

Appendix A2 – Grid layer creation:

1. We created a grid that occupied the entire length of our project ("Creating Vectors" > "Creating Grid"): "Grid Type": Rectangle (polygon); "Grid Extension": -180.000000000,180.000000000,-90.000000000,83.634100653 [EPSG: 4326] (Layer: *ADMIN*); "Horizontal spacing" and "Vertical spacing": 0.09000900090009000900090009; "Horizontal overlay" and "Vertical overlay": 0.0000; "Grid SRC": EPSG: 4326 – WGS 84. We saved the grid as a temporary layer, which consisted of a total of 7.720.000 cells of 0,09 x 0,09 geographical degrees. Every cell contained an *id*, *left*, *top*, *right* and *bottom* attributes.
2. We then clipped this grid for every GMR layer. We used "Select by location" tool with "Select objects from": Grid [EPSG: 4326]; "Where objects (geometric predicate)": intersect; "Comparing with objects of": [GMR layer] [EPSG: 4326]; "Modify the current selection by": creating a new selection. Every selection was exported to ESRI Shape File (e.g., *grid10_cape.shp*). The resulting subset layers that we eventually used in this study were: *grid10_cape*, *grid10_caucasus*, *grid10_himalaya*, *grid10_greatdividing*, *grid10_alps*, *grid10_iberian*, *grid10_scandinavian*, *grid10_UKranges*, *grid10_appalachian*, *grid10_centralamerica*, *grid10_rockies* and *grid10_andes*.

3. We marged all single grid layers into a single temporary layer (using “Merge vector layers” tool). We then used “Join attributes by location” tool, to add *Continent*, *GMR*, *Mountain Name* and *ID_mountain* attributes to every cell (also using a single temporary combined layer of the GMRs we needed): “Base layer”: [temporary combined grid layer in EPSG: 4326]; “Join layer”: [temporary combined GMRs layer in EPSG: 4326]; “Geometric predicate”: intersects, “Fields to add”: *Name*, *Continent*, *ID_mountai*, *GMR*; “Type of union”: Take attributes of the feature with largest overlap only (one-to-one)”. The resulting file layer was: *grid10global_withinfo*.

Appendix A3 – Habitat and DEM layers creation:

1. We loaded the raster layer *glc_shv10_DOM* (Latham et al., 2014) as follows: “Layer” > “Add layer” > “Add raster layer”: *glc_shv10_DOM*. We made sure it was on EPSG: 4326 – WGS 84 using the “Raster” tool > “Projections” > “Assign Projection”.
2. We executed “Raster” > “Extraction” > “Cut raster by extension”; we filled “Input layer”: *glc_shv10_DOM*; “Cut extension”: *GMBA_MI_with_IDm_GMR* [EPSG: 4326] and clicked “Run”. The resulting layer *Cropped (extension)* was trimmed again using “Raster” > “Extraction” > “Cut raster by mask layer”; we filled “Input layer”: *Cropped (extension)* [EPSG: 4326], “Mask layer”: *GMBA_MI_with_IDm_GMR* [EPSG: 4326], “Source SRC”: EPSG: 4326 – WGS 84, “Target SRC”: EPSG: 4326 – WGS 84, and we selected “Adjust the extension of the cut raster to the extension of the mask layer”. The resulting layer was saved as: *glc_hab_gmr*.
3. Then, we used “Raster pixels to points” tool as follows: “Raster layer”: *glc_hab_gmr* [EPSG: 4326]; “Band number”: Band 1 (Gray); “Field name”: VALUE and clicked “Run”. As a result, we obtained the temporary layer *Vector Points*, and we created a spatial index for this layer.
4. We finally clipped the vectorial layer *Vector Points* with every included GMR vector layer, and we obtained 15 subset layers of vectorial points (e.g., *glc_cape*) – that contained specific habitat information. To do this, we used the “Select by location” tool (as we have explained in Appendix A2). To verify that the exported layers were created correctly, we used “Merge Vector Layers” – so we confirmed that we had not lost data during this process: the total number of objects in the new layer was equal to the original layer. We did not use all these layers to create the final maps.
5. We repeated the same processes with DEM layer (*DEM_geotiff*; *ETOPO5*).

Appendix A4 ⚠

The full reproducible code used to create the maps and obtain CIMPAL scores, StCIMPAL scores, average elevations per cell, IASs richness per cell, and subsequent statistical analyses is available at the following link:

https://www.mediafire.com/folder/a0e9e71110xii/Appendix_TFM_JRJ_MappingTheImpactOfInvasiveAlienSpeciesOnMountainEcosystems

Appendix A5 – Conversion of GBIF geospatial data (CSV documents) to occurrence points in ESRI Shapefile format:

1. For each selected IAS, we downloaded – in CSV format – the occurrence data recorded in its corresponding C-GMRs.
2. Next, we imported all the CSV files – one by one – into QGIS 3.16.4. Hannover (QGIS Development Team, 2021), following the procedure below:
   2.1. To load each CSV file, we opened “Data Source Manager | Delimited text” through the top menu “Layer” > “Add layer” > “Add layer of delimited text…”.
   2.2. We clicked on the “…” button (next to “File Number”) and entered the path to the CSV text file. We used UTF-8 encoding.
   2.3. In the “File Format” section, we selected “Custom Delimiters” and checked “Tab”.

2.4. In the "Record and field options" section, we selected "The first record has the field names" and "Detect field types". We left the "Number of header lines to discard" at 0.

2.5. In the "Geometry Definition" section, we selected the "Point Coordinates" option and filled in the "Field X" and "Field Y" columns with *decimalLongitude* and *decimalLatitude*, respectively. Then we selected the SRC EPSG geometry: 4326 – WGS 84 and clicked "Add".

3. We exported – one by one – the CSV layers of points (imported) to ESRI Shapefile format. For each layer:

3.1. We right-clicked on the layer and selected "Export" > "Save object as".

3.2. In the drop-down menu "Save vector layer as …", we selected "Format" > "ESRI shapefile" and "SRC > EPSG: 4326 – WGS 84".

3.3. In the "Select fields to export and their export options" section we left all the options marked by default.

3.4. In the "Geometry" section, we selected "Automatic" and clicked "OK".

4. Through these procedures, we obtained all occurrence records in ESRI Shapefile format.

Appendix A6 – First point filtering process. Selection of occurrence points that intersected with the mountain polygons:

1. We intercepted – one by one – all the occurrence points layers (both group A and B) with their corresponding GMR polygon layers – to select only the occurrence points that fell within mountainous areas. For example, we intercepted the *GroupA_Alps* points layer (formed by occurrence points of group A species in the C-GMRs that make up the Alps – Carpathians – Balkans zone) with the *Alps – Carpathians – Balkan* GMR layer, resulting in a filtered layer (*GrupA_Alps_filtered*), formed only by the occurrence points located in this GMR.
2. We selected the points of interest as follows: "Vector" > "Research tools" > "Select by location"; then we filled in the different parameters: "Select objects from": *GrupA_Alps* [EPSG: 4326]); "Where objects (geometric predicate)": intersect; "Comparing with the objects of": *Alps – Carpathians – Balkans* [EPSG: 4326]; "Modify current selection by": creating a new selection. Once the process was complete, we double-clicked on the *GrupA_Alps* layer [EPSG: 4326] and clicked on "Export" > "Save selected objects as…" and saved the selected points in ESRI Shapefile format (in SRC EPSG: 4326 – WGS 84, UTF-8).

Appendix A7 – Second point filtering process. Selection of group B occurrence points (excluding points located within natural distribution areas):

Through the filtered layers of group B, we visualized – one by one – whether the occurrence points of each species fell within their natural areas of distribution (sometimes using maps or other resources as support). In cases where it was obvious that they were in non-native areas, we did not remove any points; while to deal with the records of the most heterogeneous layers, we proceeded as follows:

1. For each of the problematic species, we downloaded (in JPEG, PNG, or TIFF format) its distribution map (s), which were to indicate the native and non-native areas.
2. Using the "Georeferencing" tool, we projected all the maps of interest on our QGIS project – using the ADMIN layer as the base map. To georeference each map, we proceeded as follows: we went to the "Raster" menu > "Georeferencer" and clicked on the icon "Open raster". In the dialog we selected the directory of each image and clicked on the "Open" button. We then selected the points in the image that we wanted to use as a reference and the "Enter Map Coordinates" dialog box opened. We worked manually (using the "From the map canvas" option) and selected the points in the ADMIN layer that we thought best matched the reference points in the image (this will automatically fill in the "X/East" and "Y/North" fields), and we clicked "OK". After repeating this process for several points in each image, we clicked the "Start georeferenced" button. In this case, the "Transformation Configuration" dialog box opened, in which we filled in the following sections (Transformation Parameters and

Output Settings): “Transformation Type”: Linear, “Removal Method”: Nearest Neighbour, “Destination SRE”: EPSG: 4326 – WGS 84, “Output raster”: [desired name and destination], “Compression”: None. We clicked the “Upload to QGIS when done” option and clicked “OK”. Once loaded into QGIS, we made sure that dX and dY (pixels) were less than 8 (which was a good way to tell us that the georeferencing process was accurate). If the image was not well projected on the base map, we repeated the process, adding georeferenced points – until we got a well georeferenced image.

3. Once we had the desired maps and they were loaded into the project, we loaded the corresponding point layers (as explained above). In edit mode and using the “Select objects by area or single click” tool, we eliminated – for each problematic species – the points that fell within the natural areas of distribution (Figure A7.1 and Figure A7.2). In all cases we kept control layers in case we had to make modifications to the resulting layers. It should be noted how we worked with the margins between native and non-native areas (see next page).

Figure A6.1. This images represents the process of elimination points on borders between native and non-native areas – specifically in the case of *Pinus mugo* in Europe (left) and *Oncorhynchus aguabonita* in North America (right). The georeferenced maps describing the native areas are from Ballian et al. (2016) and USGS, respectively. Grey lines: borders between countries (base map). Orange lines (left): borders between countries (georeferenced image). Green area (left) and orange area (right): native distribution. Brown area (right): non-native distribution. Big blue points: *Pinus mugo* occurrences reported by the National Forest Inventories. Yellow points: eliminated points (native). Red points: included points (non-native).

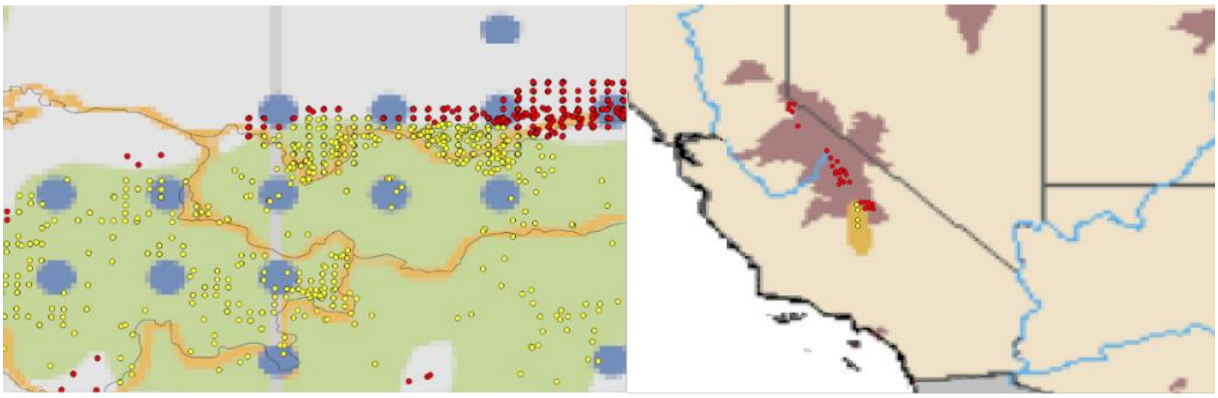
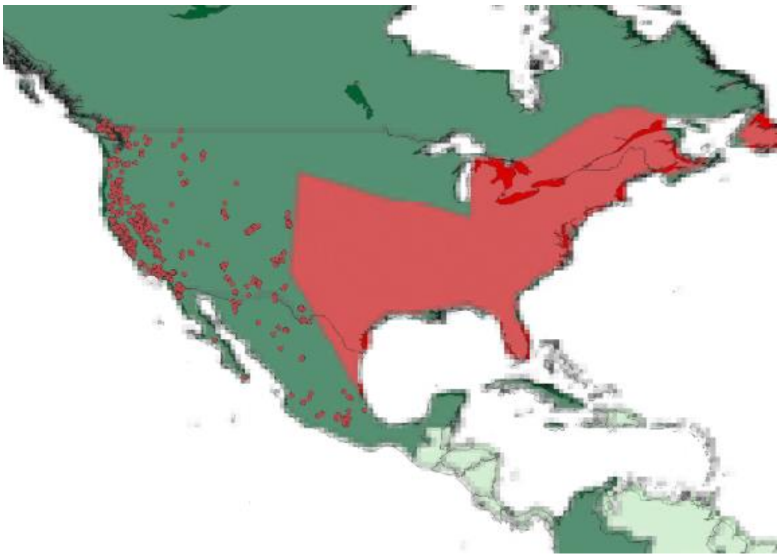


Figure A6.2. Point selection process for *Lithobates catesbeianus* in the Rocky Mountains (North America). In this case we were able to perfectly georeferene the map of native (red) and non-native (dark green) distribution areas; we didn’t have to remove any occurrence points as they were all outside the native area.



Appendix A8 – Combining point layers:

1. In the QGIS menu, we selected “Vector” > “Data management tools” > “Merge vector layers…”. Then appeared the window “Merge vector layers”, where we chose the layers that we were interested in joining (all the layers of filtered occurrence points; a total of 34 input layers). We selected Project CRS: EPSG: 4326 – WGS 84 as the target SRC. Finally, we created the combined layer as a permanent file (*all_records* [EPSG: 4326]) and selected “OK”. The resulting layer contained all occurrence points joined.
2. We removed the following attribute columns from the resulting layer, as we were not required for our study: *occurrence*, *infraspeci*, *taxonRank*, *verbatimSc*, *verbatim_1*, *locality*, *occurren_1*, *StateProvi*, *individual*, *publishing*, *eventDate*, *coordinate*, *coordina_1*, *elevationA*, *depth*, *depthAccur*, *day*, *month*, *institution*, *collection*, *catalogNum*, *recordNumb*, *identified*, *dateIdenti*, *rightsHold*, *recordedBy*, *establishm*, *mediaType*, *basisOfRec*, *typeStatus*, *lastInterp* and *issue*.
3. We loaded and merged all the GMR layers into a single temporary layer (using “Merge vector layers” tool), which allowed us to add the GMR field to the GMBA Mountain Inventory layer (using “Join attributes by location”), such as and as explained below with other fields.*
4. We assigned to each point the name, ID, GMR and continent of the mountainous region where it was located: “Vector” → “Data management tools” → “Join attributes by location”: “Base Layer”: *all_records* [EPSG: 4326]; “Join layer: *GMBA Mountain Inventory* [EPSG: 4326]; “Geometric predicate”: intersects, “Fields to add”: *Name*, *Continent*, *ID_mountai*; “Type of union”: Take only the attributes of the first matching object (one by one); “United field prefix”: *mountain_*. The resulting file layer (Run) was *all_records_IDm_GMR*.*
5. We then assigned the ID of each cell to each of the points in the *all_records_IDm_GMR* layer, using the “Join Attributes by Location” tool. We saved the resulting layer as *all_records_IDm_GMR_IDcel*, performing as “Type of union”: Take only the attributes of the first matching object (one by one)”. To speed up this procedure we created a spatial index for both layers using “Layer Properties” > “Font” > “Geometry” > “Create Spatial Index”.*

* These last three steps were ultimately redundant as we performed similar steps with RStudio (R Core Team, 2021). In any case, they helped us to verify that the procedures performed with this latest software were correct.

Table A1 – GMR layers (20), based on Grêt-Regamey and Weibel (2020) and other geomorphological maps from IAS PMF.

Continent	GMR layer	GMR abbreviation	Number of polygons
Africa	Atlas	ATL	10
Africa	Cape Ranges – Drakensberg - Kalahari	CRDK	30
Africa	Eastern Arc Mountains – Ethiopian Highlands	EAMEH	40
Africa	Madagascar	MAD	4
Asia	Himalaya	HIM	180
Asia	Japanese Ranges	JR	10
Asia	Siberian Plateau	SIBP	135
Asia	Tropical East Asia Ranges	TEAR	38
Australia	Great Dividing Range – Southern Alps	GDRSA	51
Europe	Alps – Carpathians – Balkans	ACB	34
Europe	Caucasus Ranges	CAUR	103
Europe	Iberian Peninsula Mountain Ranges - Canarias	IPMR	13
Europe	Scandinavian Ranges	SCAR	3
Europe	UK Ranges	UKR	7
North America	Appalachian Mountains	APP	3
North America	Central America Ranges – Hawaii	HAWCA	50
North America	Greenland	GREE	5
North America	Rocky Mountains	RM	218
South America	Amazonas Rainforest – The Pampas	ARTP	51
South America	Andes	AND	63

Table A2 – List of C-GMRs.

GMR	C-GMRs
ACB	Albania, Austria, Bosnia and Herzegovina, Bulgaria, Croatia, Corsica, Czech Republic, France, Germany, Greece, Hungary, Italy, Kosovo, Liechtenstein, Macedonia, Monaco, Montenegro, Poland, Romania, Sardinia, Serbia, Slovenia, Switzerland, Ukraine.
AND	Argentina, Bolivia, Colombia, Chile, Ecuador, Peru, Venezuela, Trinidad.
APP	Canada, USA.
CRDK	Angola, Namibia, South Africa.
CAUR	Azerbaijan, Cyprus, Georgia, Iran, Iraq, Israel, Jordan, Lebanon, Oman, Pakistan, Russia, Oman, Saudi Arabia, Syria, Turkey, United Arab Emirates, USA, Yemen.
HAWCA	Belize, Colombia, Costa Rica, Cuba, Dominican Republic, El Salvador, Guatemala, Haiti, Honduras, Jamaica, Mexico, Nicaragua, Panama, USA.
EAMEH	Burundi, Cameroon, Congo, Ethiopia, Guinea, Ivory Coast, Kenya, Malawi, Mozambique, Nigeria, Rwanda, South Sudan, Sudan, Tanzania, Uganda, Zambia, Zimbabwe.
GDRSA	Australia, New Zealand.
HIM	Afghanistan, Bhutan, Cambodia, China, India, Kazakhstan, Kyrgyzstan, Laos, Myanmar, Nepal, Pakistan, Afghanistan, Sri Lanka, Taiwan, Tajikistan, Thailand, Turkmenistan, Uzbekistan, Vietnam.
IPMR	Andorra, France, Portugal, Spain.
JR	Japan.
RM	Alaska, Canada, Mexico, USA.
SCAR	Finland, Norway, Svalbard, Sweden.
SIBP	China, Kazakhstan, Mongolia, North Korea, South Korea, Novaya Zemlya, Russia.
UKR	England, Ireland.
MAD	No countries compiled.
ATL	No countries compiled.
TEAR	No countries compiled.
GREE	No countries compiled.
ARTP	No countries compiled.

APPENDIX B ⚠

Table B1 – Final list of publications included and excluded in this study after the first and second scanning, selection, and review processes. The list with basic information of the first 245 articles obtained from ISI Web of Knowledge (List B1) and the information extracted from each publication through the first scan (List B2) are available at the following link:
https://www.mediafire.com/folder/a0e9e71110xii/Appendix_TFM_JRJ_MappingTheImpactOfInvasiveAlienSpeciesOnMountainEcosystems

Reference	Included / Excluded	Reason for exclusion
Acevedo and Cassinello, 2009	Excluded (first round)	General information
Alexander et al., 2009	Excluded (first round)	General information
Allen et al., 2007	Excluded (first round)	General information
Alston and Richardson, 2006	Excluded (first round)	General information
Ansong and Pickering, 2014	Excluded (first round)	General information
Aplet et al., 1998	Excluded (first round)	General information
Arismendi et al., 2012	Excluded (first round)	General information
Arteaga et al., 2009	Excluded (first round)	General information
Becker et al., 2005	Excluded (first round)	General information
Belote and Jones, 2009	Excluded (first round)	General information
Berger, 2007	Excluded (first round)	General information
Bomhard et al., 2005	Excluded (first round)	General information
Brinkman and Hundertmark, 2009	Excluded (first round)	General information
Burke, 2003	Excluded (first round)	General information
Chytrý et al., 2008	Excluded (first round)	General information
Cutler and Swann, 1999	Excluded (first round)	General information
Dana et al., 2011	Excluded (first round)	General information
Dana et al., 2014	Excluded (first round)	General information
Ellsworth et al., 2016	Excluded (first round)	General information
Gritti et al., 2006	Excluded (first round)	General information
Guo et al., 2018	Excluded (first round)	General information
Haider et al., 2018	Excluded (first round)	General information
Hawbaker and Radeloff, 2004	Excluded (first round)	General information
Hemp, 2008	Excluded (first round)	General information
Higgins et al., 1997	Excluded (first round)	General information
Hulme et al., 2013	Excluded (first round)	General information
Iannone et al., 2016	Excluded (first round)	General information
Jaeger et al., 2008	Excluded (first round)	General information
Khuroo et al., 2011	Excluded (first round)	General information
Kloppers et al., 2005	Excluded (first round)	General information
Kueffer et al., 2013	Excluded (first round)	General information

Reference	Included / Excluded	Reason for exclusion
Laurence and Andersen, 2003	Excluded (first round)	General information
Le Roux and McGeoch, 2008	Excluded (first round)	General information
McDougall et al., 2011a	Excluded (first round)	General information
McDougall et al., 2011b	Excluded (first round)	General information
Melo-Ferreira et al., 2009	Excluded (first round)	General information
Moore et al., 2011	Excluded (first round)	General information
Mount and Pickering, 2009	Excluded (first round)	General information
Nuñez et al., 2008	Excluded (first round)	General information
Oduor et al., 2016	Excluded (first round)	General information
Okabe and Goka, 2008	Excluded (first round)	General information
Ortega et al., 2014	Excluded (first round)	General information
Otfinowski and Kenkel, 2008	Excluded (first round)	General information
Paiaro et al., 2007	Excluded (first round)	General information
Pauchard et al., 2009	Excluded (first round)	General information
Pauchard et al., 2013	Excluded (first round)	General information
Pauchard et al., 2016	Excluded (first round)	General information
Pérez et al., 2009	Excluded (first round)	General information
Perry et al., 2018	Excluded (first round)	General information
Polidori et al., 2018	Excluded (first round)	General information
Rahel et al., 2008	Excluded (first round)	General information
Richardson et al., 1996	Excluded (first round)	General information
Richardson et al., 2007	Excluded (first round)	General information
Rija et al., 2014	Excluded (first round)	General information
Romain-Bondi et al., 2004	Excluded (first round)	General information
Rossell et al., 2014	Excluded (first round)	General information
Rowe et al., 2007	Excluded (first round)	General information
Roy et al., 2009	Excluded (first round)	General information
Sada et al., 2005	Excluded (first round)	General information
Seipel et al., 2012	Excluded (first round)	General information
Simpson and Prots, 2013	Excluded (first round)	General information
Siniscalco and Barni, 2018	Excluded (first round)	General information
Sinkins and Otfinowski, 2012	Excluded (first round)	General information
Tecco et al., 2016	Excluded (first round)	General information
Telcean et al., 2017	Excluded (first round)	General information
Turpie et al., 2003	Excluded (first round)	General information
Turpie et al., 2008	Excluded (first round)	General information
Val et al., 2016	Excluded (first round)	General information

Reference	Included / Excluded	Reason for exclusion
van Wilgen, 2012	Excluded (first round)	General information
Ventura et al., 2017	Excluded (first round)	General information
Wells et al., 2012	Excluded (first round)	General information
Zalewski et al., 2009	Excluded (first round)	General information
Ammunét et al., 2011	Included	Not excluded
Amodeo and Zalba, 2013	Included	Not excluded
Auger-Rozenberg et al., 2012	Included	Not excluded
Barrios-Garcia et al., 2014	Included	Not excluded
Bates et al., 2011	Included	Not excluded
Bonelli et al., 2017	Included	Not excluded
Boughton and Boughton, 2014	Included	Not excluded
Brantley et al., 2013	Included	Not excluded
Brantley et al., 2015	Included	Not excluded
Brown et al., 2008	Included	Not excluded
Brummer et al., 2016	Included	Not excluded
Bucciarelli et al., 2019	Included	Not excluded
Caravaggi et al., 2015	Included	Not excluded
Carlsson et al., 2010	Included	Not excluded
Cayuela et al., 2013	Included	Not excluded
Chang et al., 2018	Included	Not excluded
Coetsee and Wigley, 2013	Included	Not excluded
Coleman and Levine, 2007	Included	Not excluded
Combs et al., 2011	Included	Not excluded
Convey et al., 2011	Included	Not excluded
Crespo-Pérez et al., 2011	Included	Not excluded
Curry et al., 2016	Included	Not excluded
Dale and Adams, 2003	Included	Not excluded
Dehlin et al., 2008	Included	Not excluded
Dong et al., 2011	Included	Not excluded
Edward et al., 2009	Included	Not excluded
Enoki and Drake, 2017	Included	Not excluded
Esler et al., 2010	Included	Not excluded
Feldhaus et al., 2013	Included	Not excluded
Flesch et al., 2016	Included	Not excluded
Gao et al., 2018	Included	Not excluded
García-Díaz et al., 2013	Included	Not excluded
Giantomasi et al., 2008	Included	Not excluded

Reference	Included / Excluded	Reason for exclusion
Gross, 2001	Included	Not excluded
Hazelton and Grossman, 2009	Included	Not excluded
Heard and Valente, 2009	Included	Not excluded
Henn et al., 2016	Included	Not excluded
Higgins et al., 2001	Included	Not excluded
Hilty et al., 2006	Included	Not excluded
Holmes, 2002	Included	Not excluded
Hoxmeier and Dieterman, 2016	Included	Not excluded
Hua et al., 2011	Included	Not excluded
Iwai and Shoda-Kagaya, 2012	Included	Not excluded
Kalinowski et al., 2010	Included	Not excluded
Kašák et al., 2015	Included	Not excluded
Kats et al., 2013	Included	Not excluded
Kerby et al., 2005	Included	Not excluded
Kiełtyk and Delimat, 2019	Included	Not excluded
Kizlinski et al., 2002	Included	Not excluded
Kleinbauer et al., 2010	Included	Not excluded
Krapfl et al., 2012	Included	Not excluded
Laube et al., 2015	Included	Not excluded
Laushman et al., 2018	Included	Not excluded
Lepori et al., 2012	Included	Not excluded
Loewen and Vinebrooke, 2016	Included	Not excluded
Luja and Rodríguez-Estrella, 2010	Included	Not excluded
Lynch, 2004	Included	Not excluded
Maclennan et al., 2015	Included	Not excluded
Marshal et al., 2008	Included	Not excluded
Masumbuko et al., 2012	Included	Not excluded
Messner et al., 2013	Included	Not excluded
Milligan et al., 2017	Included	Not excluded
Miró and Ventura, 2015	Included	Not excluded
Miró et al., 2018	Included	Not excluded
Molina-Montenegro et al., 2009	Included	Not excluded
Molina-Montenegro et al., 2012	Included	Not excluded
Muhlfeld et al., 2017	Included	Not excluded
Ni et al., 2010	Included	Not excluded
Olsen and Belk, 2005	Included	Not excluded
Olsson et al., 2012	Included	Not excluded

Reference	Included / Excluded	Reason for exclusion
Orlova-Bienkowskaja and Bieńkowski, 2017	Included	Not excluded
Orwig et al., 2012	Included	Not excluded
Parker et al., 2001	Included	Not excluded
Pauchard, 2003	Included	Not excluded
Pearson and Goater, 2008	Included	Not excluded
Petryna et al., 2002	Included	Not excluded
Pickering and Hill, 2007	Included	Not excluded
Pollnac et al., 2014	Included	Not excluded
Pope et al., 2008	Included	Not excluded
Prévosto et al., 2006	Included	Not excluded
Price and Weltzin, 2003	Included	Not excluded
Ransom, 2017	Included	Not excluded
Reid, 2011	Included	Not excluded
Reinhart et al., 2005	Included	Not excluded
Reinhart et al., 2006	Included	Not excluded
Relva et al., 2014	Included	Not excluded
Rissler et al., 2000	Included	Not excluded
Sacks et al., 2016	Included	Not excluded
Salinas et al., 2015	Included	Not excluded
Schlichting et al., 2015	Included	Not excluded
Schreuder and Clusella-Trullas, 2016	Included	Not excluded
Shelton et al., 2016	Included	Not excluded
Smith et al., 2015	Included	Not excluded
Snyder et al., 2011	Included	Not excluded
Soto et al., 2006	Included	Not excluded
Stevenson-Holt and Sinclair, 2015	Included	Not excluded
Straube et al., 2009	Included	Not excluded
Sugiura et al., 2013	Included	Not excluded
Tabor et al., 2015	Included	Not excluded
Tanentzap et al., 2009	Included	Not excluded
Tomiolo et al., 2016	Included	Not excluded
Urban et al., 2006	Included	Not excluded
Urban et al., 2009	Included	Not excluded
Urban et al., 2013	Included	Not excluded
Van Der Waal et al., 2012	Included	Not excluded
van Riper et al., 2010	Included	Not excluded
Kanno et al., 2017	Excluded (while extracting data)	Not suitable

Reference	Included / Excluded	Reason for exclusion
Nierbauer et al., 2016	Excluded (while extracting data)	Not suitable
Alexander et al., 2005	Excluded (second round)	Not suitable
Crooks et al., 2008	Excluded (second round)	Not suitable
Fleishman et al., 2006	Excluded (second round)	Not suitable
Manor and Saltz, 2004	Excluded (second round)	Not suitable
Miller and Halpern, 1998	Excluded (second round)	Not suitable
Pierce et al., 2006	Excluded (second round)	Not suitable
Restrepo and Vitousek, 2001	Excluded (second round)	Not suitable
Vergara-Tabares et al., 2018	Excluded (second round)	Not suitable
Zong et al., 2016	Excluded (second round)	Not suitable
Maitre et al., 1996	Excluded (second round)	Other reasons
McLaughlin and Bowers, 2006	Excluded (second round)	Other reasons
Pilliod et al., 2013	Excluded (second round)	Other reasons
Rosenberger et al., 2018	Excluded (second round)	Other reasons
Simberloff et al., 2010	Excluded (second round)	Other reasons
Soh et al., 2006	Excluded (second round)	Other reasons
Taft et al., 2015	Excluded (second round)	Other reasons
Thiele and Otte, 2008	Excluded (second round)	Other reasons
Williams et al., 1998	Excluded (second round)	Other reasons
Williams and Wardle, 2007	Excluded (second round)	Other reasons
Vogt et al., 2016	Excluded	Other reasons
Wang et al., 2018	Excluded	Other reasons
Wiegner et al., 2013	Excluded	Other reasons
Zhang et al., 2010	Excluded	Other reasons
Caruso et al., 2013	Excluded	Unclassified
Chambers et al., 2014	Excluded	Unclassified
Correa and Hendry, 2012	Excluded	Unclassified
Cosgriff et al., 2004	Excluded	Unclassified
Dangles et al., 2010	Excluded	Unclassified
Eads and Biggins, 2015	Excluded	Unclassified
Fill et al., 2017	Excluded	Unclassified
Gallien et al., 2015	Excluded	Unclassified
Grissino-Mayer et al., 2004	Excluded	Unclassified
Kluge and Neser, 1991	Excluded	Unclassified
Lamsal et al., 2018	Excluded	Unclassified
Macdonald and Cedex, 1991	Excluded	Unclassified
Mackey and Boone, 2009	Excluded	Unclassified

Reference	Included / Excluded	Reason for exclusion
Marcora et al., 2018	Excluded	Unclassified
Marquez et al., 2002	Excluded	Unclassified
McDougall et al., 2018	Excluded	Unclassified
Moll and Trinder-Smith, 1992	Excluded	Unclassified
Marzano et al., 2003	Excluded	Unclassified
Patten and Burger, 2018	Excluded	Unclassified
Pyšek et al., 2002	Excluded	Unclassified
Rehnus et al., 2009	Excluded	Unclassified
Ringold et al., 2008	Excluded	Unclassified
Romeiras et al., 2009	Excluded	Unclassified
Smith et al., 2012	Excluded	Unclassified
Jenkinson et al., 2016	Excluded	Unclassified
Tkacz et al., 2008	Excluded	Unclassified
van Winkel and Lane, 2012	Excluded	Unclassified
Avila et al., 2016	Excluded	Unclear classification
Elliott and Swank, 2008	Excluded	Unclear classification
Hernández-Lambraño et al., 2017	Excluded	Unclear classification
Jenkinson et al., 2016	Excluded	Unclear classification
Jules et al., 2014	Excluded	Unclear classification
Korsu et al., 2010	Excluded	Unclear classification
Ladrera et al., 2015	Excluded	Unclear classification
Lewis et al., 2017	Excluded	Unclear classification
Mendoza-Almeralla et al., 2015	Excluded	Unclear classification
Økland et al., 2011	Excluded	Unclear classification
Richardson et al., 2014	Excluded	Unclear classification
Swope and Parker, 2012	Excluded	Unclear classification
Swope et al., 2017	Excluded	Unclear classification
Tomback and Resler, 2007	Excluded	Unclear classification
Tomback et al., 2016	Excluded	Unclear classification

Table B2 –

The IASs inventory with all data collected (**Table B2**) is available at the following link:

https://www.mediafire.com/folder/a0e9e71110xii/Appendix_TFM_JRJ_MappingTheImpactOfInvasiveAlienSpeciesOnMountainEcosystems

Table B3 – List of the 130 IASs collected in this study. The names of the species are those obtained directly from the publications and are therefore not standardized. *: species we excluded because GBIF database did not have occurrence records in the C-GMRs we had selected; **: species we excluded through visual assessment. Underlined species were associated with high impacts ($\Sigma w_i > 0$). [A]: species from group A. [B]: species from group B. [+]: species from both groups (A and B). The complete tables with the AHWG matrices are available at the following link:

https://www.mediafire.com/folder/a0e9e71110xii/Appendix_TFM_JRJ_MappingTheImpactOfInvasiveAlienSpeciesOnMountainEcosystems

Acacia cyclops[A]	_Cryptolaemus montrouzieri_	_Lotus corniculatus_	***Procambarus clarkii***[B]
Acacia mearnsii[A]	***Cytisus scoparius***[B]	***Lotus unifoliolatus***[B]	_Prunus mahaleb_
Acacia saligna[A]	_Dactylis glomerata_	***Lumbricus rubellus***[A]	***Pseudotsuga menziesii***[A]
Acer platanoides[A]	***Dama dama***[A]	***Lumbricus terrestris***[A]	***Psidium cattleianum***[B]
Achillea millefolium	_Daucus carota_	_Megastigmus schimitscheki_	***Pyracantha angustifolia***[A]
Adelges tsugae[A]	***Dendrobaena octaedra***[A]	_Melica przewalskyi_*	_Rhaponticum repens_[A]
Ageratum conyzoides[A]	_Didelphis virginiana_	***Melilotus officinalis***[A]	_Rhyzobius lophantae_
Agriopis aurantiaria[B]	***Elatobium abietinum***[A]	_Merizodus soledadinus_*	***Robinia pseudoacacia***[A]
Agrostis capillaris	***Equus asinus***[A]	_Metaphire hilgendorfi_*	_Rumex acetosella_
Alternanthera philoxeroides[A]	***Erigeron annuus***[A]	_Mirabilis jalapa_	***Salmo spp (Salmo trutta)***[+]
Amaranthus retroflexus	_Erigeron bonariensis_	***Neovison vison***[A]	***Salvelinus fontinalis***[+]
Ambrosia artemisiifolia	***Erigeron canadensis***[A]	***Notropis lutipinnis***[B]	***Salvelinus namaycush***[B]
Amynthas agrestis[A]	_Erigeron sumatrensis_	***Octolasion tyrtaeum***[A]	_Sciurus carolinensis_
_Amynthas tokioensis_*	_Euphorbia supina_	***Oenothera glazioviana***[A]	_Serangium montazerii_
Anthoxanthum odoratum	_Festuca pratensis_[A]	***Oncorhynchus aguabonita***[B]	_Sericostachys scandens_*
Aporrectodea spp[A]	***Galinsoga parviflora***[A]	***Oncorhynchus clarkii***[B]	_Solidago canadensis_
Avena barbata[A]	***Geranium carolinianum***[A]	***Oncorhynchus mykiss***[+]	***Spiraea japonica***[A]
Bidens frondosa	***Hakea sericea***[A]	_Operophtera brumata_[B]	***Sus scrofa***[A]
Bidens pilosa[A]	***Harmonia axyridis***[B]	***Orconectes limosus***[A]	***Symphyotrichum subulatum***[A]
Bromus diandrus[A]	_Herpestes javanicus_**	***Oreamnos americanus***[B]	_Syzygium jambos_
Bromus hordeaceus[A]	***Hippodamia variegata***[A]	_Oxychilus alliarius_[A]	***Taraxacum officinale***[A]
Bromus madritensis[A]	***Holcus lanatus***[A]	_Pelophylax ridibundus_	_Tecia solanivora_
Bromus tectorum[A]	***Hypochaeris radicata***[A]	_Peperomia pellucida_	_Trechisibus antarcticus_*
Castor canadensis[A]	***Impatiens glandulifera***[A]	_Phleum pratense_	***Trifolium pratense***[A]
_Casuarina equisetifolia_*	***Impatiens parviflora***[A]	***Phoxinus phoxinus***[B]	***Trifolium repens***[A]
Cenchrus ciliaris[A]	***Juniperus occidentalis***[B]	***Phytolacca americana***[A]	_Utricularia inflata_[B]
Cervus canadensis[B]	_Lepidium didymum_	***Pinus contorta***[A]	_Verbascum thapsus_
Cervus elaphus[A]	***Lepus europaeus***[B]	***Pinus mugo***[B]	***Veronica hederifolia***[A]
Cirsium vulgare[A]	***Lespedeza cuneata***[A]	***Pinus pinaster***[A]	***Veronica persica***[B]
_Cordia alliodora_*	_Linaria dalmatica_	***Pinus radiata***[A]	***Virgilia divaricata***[B]
_Coreopsis grandiflora_*	***Linaria vulgaris***[A]	***Plantago lanceolata***[A]	***Vulpes vulpes***[A]
Cottus asper[B]	***Lithobates catesbeianus***[B]	***Plantago virginica***[A]	
Crassocephalum crepidioides[A]	_Lolium multiflorum_	_Plethodon jordani_[B]	

Table B4 – ⚠

The AHWG matrix in long format (**Table B4)** is available at the following link:

https://www.mediafire.com/folder/a0e9e71110xii/Appendix_TFM_JRJ_MappingTheImpactOfInvasiveAlienSpeciesOnMountainEcosystems

APPENDIX C ⚠

The consulted maps of the mountain ranges (**Appendix C1**) and distribution (**Appendix C2**) are available at the following link:

https://www.mediafire.com/folder/a0e9e71110xii/Appendix_TFM_JRJ_MappingTheImpactOfInvasiveAlienSpeciesOnMountainEcosystems

APPENDIX D

Figure D1. Correspondence table defined in Katsanevakis et al. (2016), which allows to estimate the impact weights based on the magnitude of the impact and the strength of its evidence. In our study we applied the uncertainty-averse approach, using both factors (and therefore the whole matrix) to estimate $w_{i,j}$; if the precautionary approach were to be applied, $w_{i,j}$ would only be estimated through the first line of the matrix, i.e., assuming that the strength of evidence is "robust" for all species.

w_{ij}*: impact weights for species *i* and habitat *j

		Impact				
		Minimal	Minor	Moderate	Major	Massive
Strength of evidence	Robust	0	1	2	4	8
	Medium	0	0	1	2	4
	Limited	0	0	0	1	2

Table D1. The impact magnitude classification is based on Blackburn et al. (2014) and Katsanevakis et al. (2016); instead, the categories of type of evidence follow Katsanevakis et al. (2014; 2016).

Strength of evidence	Type of study used to document impact
Robust	- Manipulative experiments (EM) - Natural experiments (EN)
Medium	- Modelling (MOD) - Direct observations (DO) - Non-experimental based correlations (CNE)
Limited	- Expert judgement (EJ)
Magnitude of impact	
Minimal	- No effect on the fitness of native species. - Negligible impact on native species due to competition, predation, parasitism, toxicity, or grazing/herbivory. - Negligible impact on ecosystem processes and functioning. - Negligible impact on keystone species or species of high conservation value. - No chemical, physical or structural impact on the ecosystem (the invasive alien species is not an ecosystem engineer).
Minor	- Reduction in individual fitness of at least one native species due to competition, predation, toxicity, or grazing/herbivory, but without causing substantial population declines. - Minor impact on ecosystem processes and functioning but without related population declines. - Negligible impact on keystone species or species of high conservation value. - The invasive alien species causes chemical, physical, or structural changes in habitat characteristics but without causing population declines in native species.
Moderate	- Decrease in populations densities of at least one native species due to competition, predation, parasitism, toxicity, or grazing/herbivory, but without causing changes in the composition of the community. - Displacement of one species of similar niche (no more than one). - Impact on ecosystem processes and functioning, resulting in declines of native populations, but without causing substantial changes in the composition of the community. - Reduction in individual fitness of at least one keystone species or species of high conservation value, but without causing decreases in their population densities. - The invasive alien species is an ecological engineer, associated with declines in the populations of native species, but without causing substantial changes in the composition of the community.
Major	- Changes in the composition of the community due to competition, predation, parasitism, toxicity, or grazing/herbivory. Local or population extinctions of at least one native species. - Impact on ecosystem processes and functioning, resulting in changes in the composition of the community. - Decrease in population densities of at least one keystone species or species of high conservation value. - The invasive alien species is an ecological engineer, associated with changes in the composition of the community. - The induced changes are reversible in the short term (less than one decade) with appropriate management measures or if the population of the invasive alien species naturally decreases.
Massive	- The same as in the "major" category but the changes produced by the invasive alien species in the ecosystem are irreversible in the short term (more than one decade), or there is currently no known effective management actions for the control of the species and it seems highly unlikely that there will be a natural decline in its populations.

Table D2. List of possible types of study, following Katsanevakis et al. (2014; 2016). Abb.: Abbreviation.

Type of study	Abb.	Description
Manipulative experiments	EM	Field or laboratory experiment that includes treatments/controls and random selection of experimental units.
Natural experiments	EN	At least one of the elements that compose manipulative experiments is not present, and the experimental units are selected by nature, i.e., not randomly.
Modelling	MOD	I.e., as derived from ecosystem models
Direct observations	DO	Direct observation or measurement of the impact – about which there is no doubt – but which is not based on experimental studies.
Non-experimental correlations	CNE	Inference based on an observed correlation between species' presence/abundance and impact, but not based on an experimental design for data collection.
Expert judgement	EJ	Usually based on empirical knowledge, the particularities of the species' traits, or through the documented impact of other similar species.

APPENDIX E

General considerations

Of the 89 species listed in the Table B3: (a) in 87 cases we obtained GBIF occurrence data at the species level, (b) in 1 case at the genus level (specifically, for *Aporrectodea* spp.) and (c) in 1 case at both levels (*Salmo* spp. in North America; *Salmo trutta* in Chile and Spain).

Specific considerations

Group A

North America

Salmo spp. it is an exotic and invasive genus – of Afro-Eurasian origin – throughout its distribution in North America; for this reason, when mapping its impact on this continent, we classified it within group A – while to map its impact in Europe, for example, we considered it within group B. Both *Salmo* spp. and *Salmo trutta* were on our list of high-impact species reported in the USA; to avoid problems of pseudo-replication and overestimation of CIMPAL scores, we decided to omit the records of *Salmo trutta* in this country – since the occurrence points of these two rates, in this country, partially coincided.

The genera *Salvelinus* spp. and *Oncorhynchus* spp. were also listed as a high-impact taxa reported in North America, as were their species *Salvelinus fontinalis, Salvelinus namaycush, Oncorhynchus aguabonita, Oncorhynchus clarkia*, and *Oncorhynchus mykiss*. In these cases, we decided to map the associated impacts only at the species level – for both Canada and the USA – because: (1) all these taxa were listed as native to the North America continent, (2) these two genera are formed by species and subspecies with high variability in distribution ranges, and (3) genus-level occurrence data included records of hybrid individuals and species with out-of-date taxonomic names.

Group B

Africa

A specific case we decided to include in the analyses was *Virgilia divaricata*; it is a native tree of South Africa, which inhabits the margins of temperate forests, but whose establishment in the adjacent patches of fynbos may be associated with an increase in soil fertility – this facilitating the expansion of forests within this other habitat (Coetsee and Wigley, 2013). To map this species in "Cape Ranges – Drakensberg – Kalahari" we considered that it generated an impact only in cells with the presence of "Shrub Covered Areas", which could be considered a precautionary approach in the absence of more specific information – regarding the exact points where the induced ecological succession described by Coetsee and Wigley (2013).

Asia and Europe: species of Eurasian origin

The species of European and Eurasian origin that we validated as invasive in all their occurrence points downloaded of Europe and Asia, and that were associated with some impact on these two continents were *Cytisus scoparius*, *Harmonia axyridis, Lepus europaeus* and *Veronica persica*. In the case of *Cytisus scoparius*, we accepted that it generated an impact in all cells with the presence of *grassland*, since Prévosto et al. (2006) defined the effect that this plant had on the flower-rich pastures of its native range. However, it would have been more appropriate to select occurrence points based on changes in land use over time – as their impact was only documented in open areas where it was not previously present (due to control exercised by grazing a few decades ago).

North America: species of American origin

The native species of North America that we validated as invasive in all their occurrence points of the American continent (and that we could associate to some impact) were: *Juniperus occidentalis*, *Lithobates catesbeianus*, *Notropis lutipinnis, Procambarus clarkii, Psidium cattleianum* and *Salvelinus fontinalis*. In the case of *Juniperus occidentalis*, we considered that it only generated impact on shrubs covered areas, according to the impact reported in Bates et al. (2011) – according to which the expansion of the original forests of this pine generates a negative effect on the sagebrush steppe.

Table E1. List of invasive alien species with associated impacts documented in the continent of which they are native (group B). We excluded occurrence registers that fell inside the native distribution range for each species. IASs: invasive alien species. IC: impacted continent. IGMR: impacted GMR. NDR: native distribution range. DNDR: detailed native distribution range. LER: location of excluded records. AM: additional maps used to extract excluded records. See Table E1 on the next page.

IASs	IC	IGMR	NDR	DNDR	LER	AM
Virgilia divaricata	Africa	Cape Ranges - Drakensberg - Kalahari	Africa	*It occurs below 1200 m ASL but from Klein Swartberg Mountains to George to Van Staden's Pass near Port Elizabeth in Eastern Cape. It occurs in forest margins, most often beside streams or on riverbanks but also on hillsides and thickets. It is found in abundance in the Knysna and Plettenberg Bay area, particularly along the Keurbooms River* (Mbambezeli and Notten, 2003).	No excluded records. We only considered that it causes an impact in Shrub Covered Areas (where it is invasive).	-
Harmonia axyridis	Asia	Caucasus Ranges	Asia	Siberia, Far East, the north-east of Kazakhstan, Mongolia, China, North Korea, South Korea, Japan, and the north of Vietnam (Orlova-Bienkowskaja and Bieńkowski, 2017).	No excluded records (Caucasus Ranges did not belong to native areas).	See Map 1 (Appendix C2).
Veronica persica	Asia	Himalaya	Western Asia	Western Asia (Dong et al., 2011): Iran, North Caucasus, Transcaucasus (Plants of The World Online).	No excluded records (Himalaya did not belong to native areas).	See Map 2 (Appendix C2).
Herpestes javanicus	Asia	Japanese Ranges	Asia	See Hays and Conant (2007).	Not considered in the analyses.	-
Cytisus scoparius	Europe	Alps - Carpathians - Balkan	Europe	See Brandes et al. (2019).	No excluded records. We only considered that it causes an impact in Grassland (invasion caused by land use changes).	-
Pinus mugo	Europe	Alps - Carpathians - Balkan	Europe	See Ballian et al. (2016).	We excluded records located in the native areas.	See Ballian et al. (2016).
Phoxinus phoxinus	Europe	Iberian Peninsula Mountain Ranges	Eurasia	*In the Iberian Peninsula it naturally occupies most of the rivers of the Cantabrian cornice – for example, in the east of Narcea River – and some of Catalonia (in the Mediterranean Basin). It is believed to be invasive in upper basin of Duero River and the Ebro River* (Lozano Rey, 1935; Doadrio, 2002).	We excluded records located in Cantabrian Mountains and Montes Vascos.	-
Salmo trutta	Europe	Iberian Peninsula Mountain Ranges	Eurasia and North Africa	It is native to the whole of the Iberian Peninsula. See (MacCrimmon and Marshall, 1968; Muhlfeld et al., 2019).	We only considered that it generates an impact in the Pyrenees (alpine region), where documented impact is described (since high mountain lakes are naturally fishless).	-

Agriopis aurantiaria	Europe	Scandinavian Ranges	Eurasia	Continental or southern areas of Norway (Ammunét et al., 2011).	We excluded the records located in Jotunheimen (southern half of the Scandinavian Ranges).	-
Operophtera brumata	Europe	Scandinavian Ranges	Eurasia	See Blackburn et al. (2020).	We excluded all records for final analysis because they belong to native distribution.	See Blackburn et al. (2020).
Lepus europaeus	Europe	UK Ranges	Eurasia and Mediter ranean	*It is native to mainland Europe except most of the Iberian Peninsula, the Mediterranean and Scandinavia, and extends east throughout the central Asian steppes. It has naturalised successfully in many countries, including Great Britain* (Flux and Angermann, 1990).	No excluded records.	-
Notropis lutipinnis	North America	Appalachian Mountains	Eastern North America	Atlantic and Gulf Slopes from Santee River, North Carolina, to Altamaha River, Georgia (Page and Burr, 1991).	We excluded records located in the native areas of Map 3 (Appendix C2).	See Map 3 (Appendix C2).
Plethodon jordani	North America	Appalachian Mountains	North America	*They are found in the Appalachian Mountains from Virginia to northern Georgia and South Carolina* (from SREL (2021)).	All record excluded.	See maps on SREL (https://srelherp.uga.edu/).
Utricularia inflata	North America	Appalachian Mountains	North America	It is native to southern and eastern North America (from CABI (2021) and USGS (2021)).	All record excluded (because all of them were located outside GMR polygons).	-
Psidium cattleianum	North America	Central America Ranges - Hawaii	South America	It is native to south-east Brazil and northern Uruguay (from CABI, 2021).	No excluded records.	Based on CABI information.
Cervus canadensis nelsoni	North America	Rocky Mountains	Asia and North America	*Its native range extends from central Asia, south to Bhutan and east to south-east Russia in a series of patchy populations, across the Bering Strait and from southern Canada to the borders of Mexico, with a population stronghold in the Rocky Mountains. This species were extirpated from the eastern states of the USA by the beginning of the 20th century but have been reintroduced to many states in recent decades* (O'Gara and Dundas, 2002; Anderson et al., 2005).	We excluded records in the blue areas of Map 4 (Appendix C2).	See Map 4 (Appendix C2).

Cottus asper	North America	Rocky Mountains	Western North America	Pacific Slope drainages from Seward, Alaska, to Ventura River, California; east of Continental Divide in upper Peace River, British Columbia (Page and Burr, 1991).	We excluded records in the native areas of Map 5 (Appendix C2). We also excluded all records of Canada.	See Map 5 (Appendix C2).
Juniperus occidentalis	North America	Rocky Mountains	Western North America	*Western juniper is native to the western United States. It is distributed from the Cascade Range in Washington east to south-eastern Idaho and south to southern Nevada and southern California* (Fryer and Tirmenstein, 2019).	No excluded records.	-
Lithobates catesbeianus	North America	Rocky Mountains	Eastern North America	*It is native to eastern North America, ranging naturally from Nova Scotia, southern Quebec, and Ontario in Canada, down through the eastern United States and Mississippi drainage, and southward along the east coast of Mexico. It has been introduced to Hawaii, parts of the western USA and Canada, Mexico and the Caribbean, South America, Europe, and Asia* (from ISSG (2005)).	No excluded records.	See Map 6.1 and Map 6.2 (Appendix C2).
Lotus unifoliolatus	North America	Rocky Mountains	West North America	Alabama, Arizona, Arkansas, British Columbia, California, Georgia, Idaho, Iowa, Louisiana, Manitoba, Mexico Northeast, Minnesota, Mississippi, Missouri, Montana, New Mexico, New York, North Carolina, North Dakota, Oregon, Saskatchewan, South Carolina, Tennessee, Texas, Washington (from Plants of the World online).	We excluded records located in the native states of Map 7 (Appendix C2).	See Map 7 (Appendix C2).
Oncorhynchus aguabonita	North America	Rocky Mountains	North America	*Endemic to Golden Trout Creek (tributary of the upper Kern River) and the upper middle and upper portions of the South Fork Kern River, Tulare and Kern counties, California* (Page and Burr, 1991).	We excluded records located in the native areas of Map 8 (Appendix C2).	See Map 8 (Appendix C2).
Oncorhynchus clarkii	North America	Rocky Mountains	North America	See Keeley et al. 2012. *Pacific Coast drainages from Prince William Sound, Alaska, to Eel River, northern California. Freshwater populations range through Rocky Mountains to Hudson Bay, Mississippi River, Great (including Lahontan, Bonneville, and Alvord basins), and Pacific basins from southern Alberta to Rio Grande drainage, New Mexico* (Page and Burr, 1991).	We excluded records located in native coastal and inland distribution, although it is likely that within these excluded areas there are also tributaries, lakes, or reservoirs with introduced populations.	Look at Figure 1 from Seiler and Keeley (2007), Figure 2 from Crawford and Muir (2008) and see Map 9 (Appendix C2).

Oncorhynchus mykiss	North America	Rocky Mountains	Asia and North America	*Pacific Slope from Kuskokwim River, Alaska, to (at least) Rio Santa Domingo, Baja California; upper Mackenzie River drainage (Arctic basin), Alberta and British Columbia; endorheic basins of southern Oregon* (Page and Burr, 1991).	We excluded records located in native coastal and inland distribution: native areas of Map 7 (Appendix C2) and black diagonal areas of Figure 7 from Crawford and Muir (2008).	Look at Map 10 (Appendix C2) and Figure 7 from Crawford and Muir (2008).
Oreamnos americanus	North America	Rocky Mountains	North America	*Its native range is the northern Rocky Mountains, the Cascade Mountains, the Coast Range from central Idaho and Washington northward to Alaska and the mountains of the Yukon and Northwest Territories* (from USDA).	We excluded records located in the native areas.	Loot at Figure 1 from Nowak et al. (2020).
Procambarus clarkii	North America	Rocky Mountains	North America	*Gulf coastal plain from the Florida panhandle to Mexico; southern Mississippi River drainage to Illinois* (from USGS (2021); Hobbs et al., 1989).	No excluded records.	See Map 11 (Appendix C2).
Salvelinus fontinalis	North America	Rocky Mountains	North America	*Most of eastern Canada from Newfoundland to western side of Hudson Bay; south in Atlantic, Great Lakes, and Mississippi River basins to Minnesota and (in Appalachian Mountains) northern Georgia* (Page and Burr, 1991).	No excluded records.	Loot at USGS Species Profile.
Salvelinus namaycush	North America	Rocky Mountains	North America	*Widely distributed from northern Canada and Alaska (missing in southern prairie provinces) south to New England and Great Lakes basin* (Page and Burr, 1991). *In north-western Montana, Lake Trout are native in Waterton Lake, Glenns Lake, Cosley Lake, and St. Mary Lake* (Snyder and Oswald 2005*). In southwestern Montana, glacial relict populations of Lake Trout exist in Elk Lake and Twin Lake* (from USGS (2021); Page and Burr, 1991).	We excluded records located in the native areas of Map 12 (Appendix C2) and most records from Canada.	See Map 12 (Appendix C2).

APPENDIX F

Appendix F1 – Differences in StCIMPAL scores between GMRs.

We compared raw and square root-transformed StCIMPAL scores by GMR (Figure F4), and in both cases GDRSA, ACB and HIM presented the highest medians of cumulative impact values (> 0.020 in raw data; ≥ 0.15 in square root-transformed data), followed by APP and UKR (> 0.010; > 0.1). On the other hand, IPMR, AND and SCAR had the lowest values (< 0.001; < 0.03), followed by HAWCA, CRDK, CAUR and RM (> 0.005; > 0.05). These results matched well with the patterns and hotspots represented in the impact maps. Pairwise comparisons using Wilcoxon rank sum test with continuity correction (*P*-value adjustment method: Bonferroni) showed significant differences between GMRs (Table F6).

Figure F1. Maps of the mountainous regions of the world with some impacted cells: E) Cape Ranges – Drakensberg, Africa; F) GDRSA, Australia and New Zealand. Most CRDK cells have low impact; in contrast, in GDRSA the vast majority are severely affected.

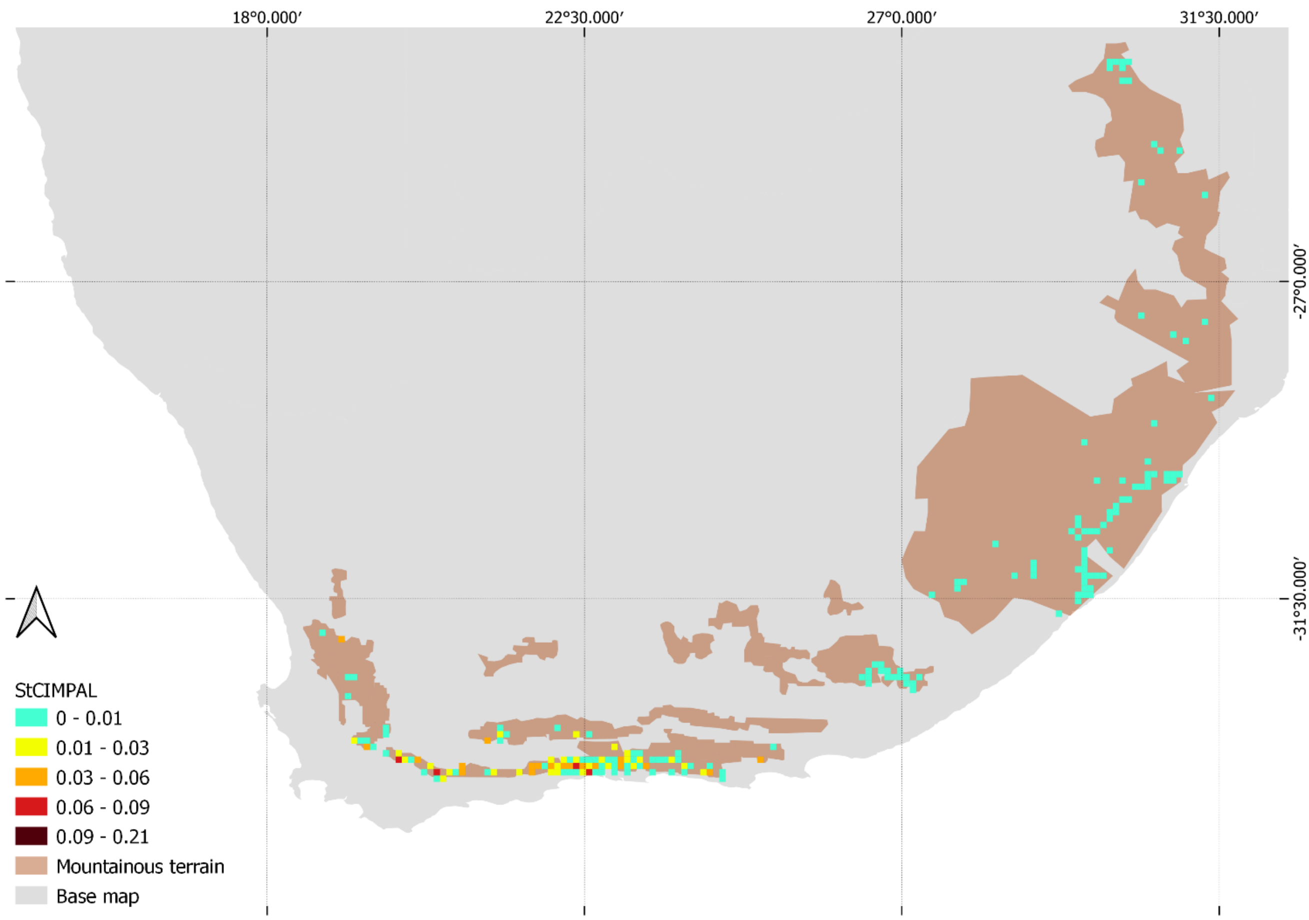
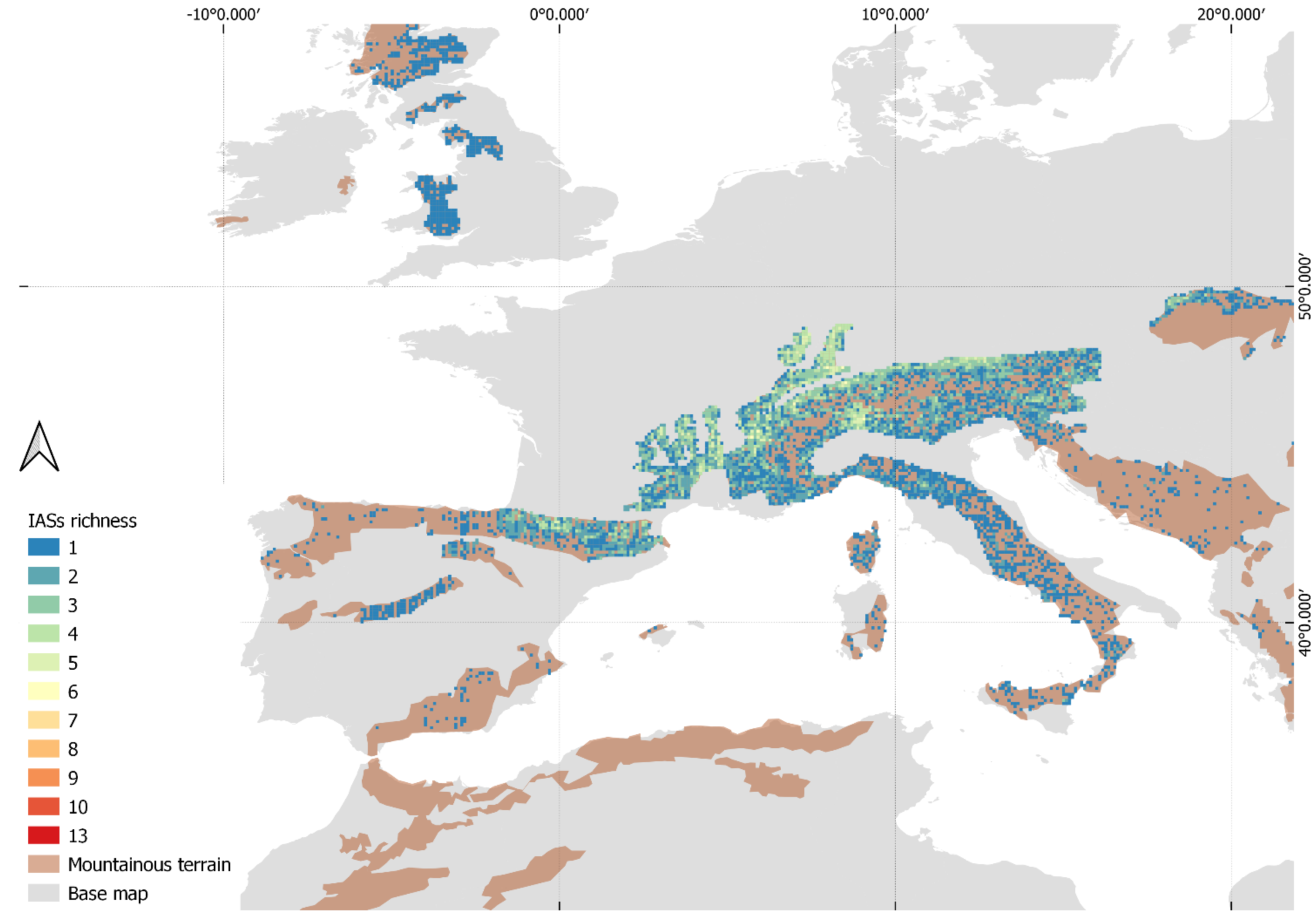
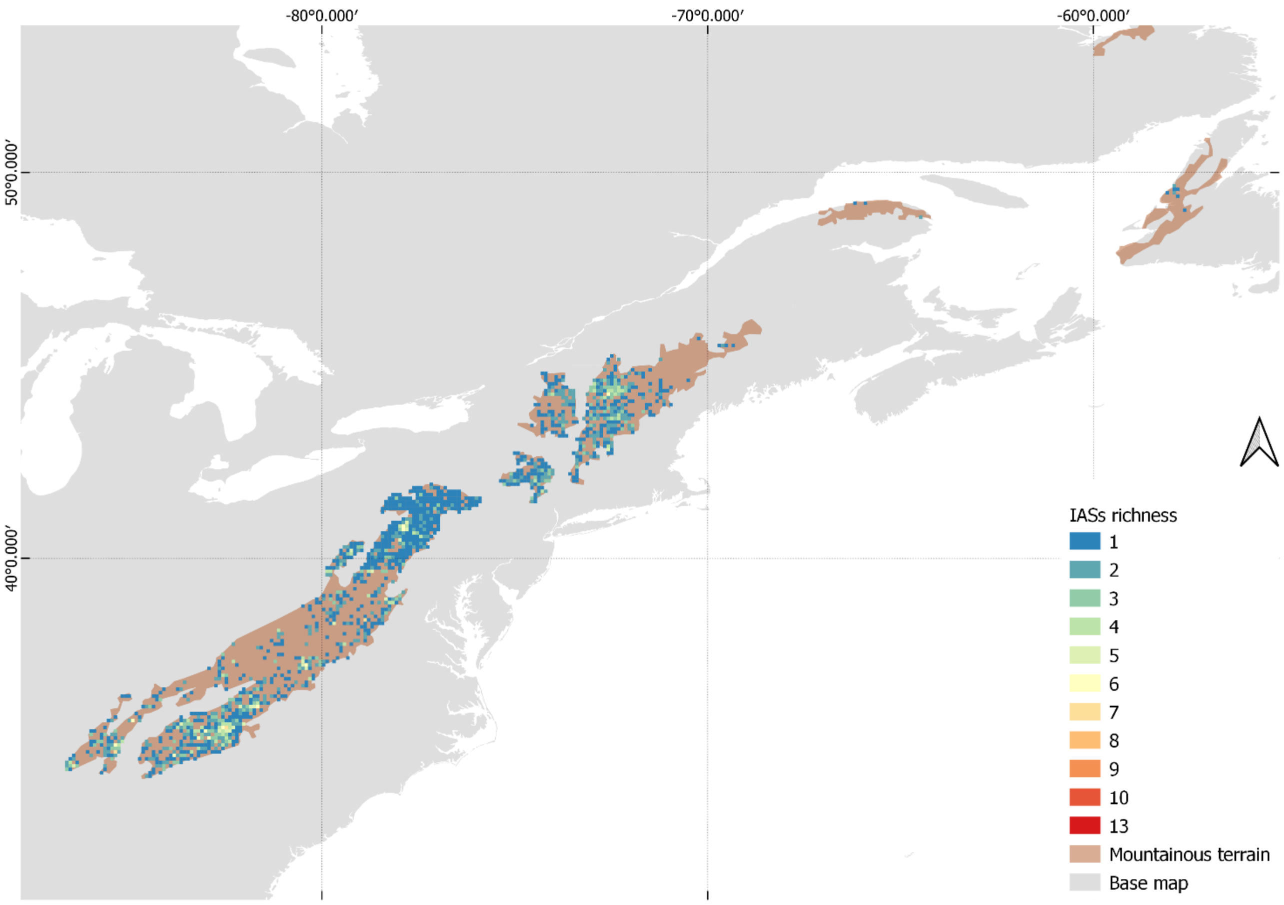
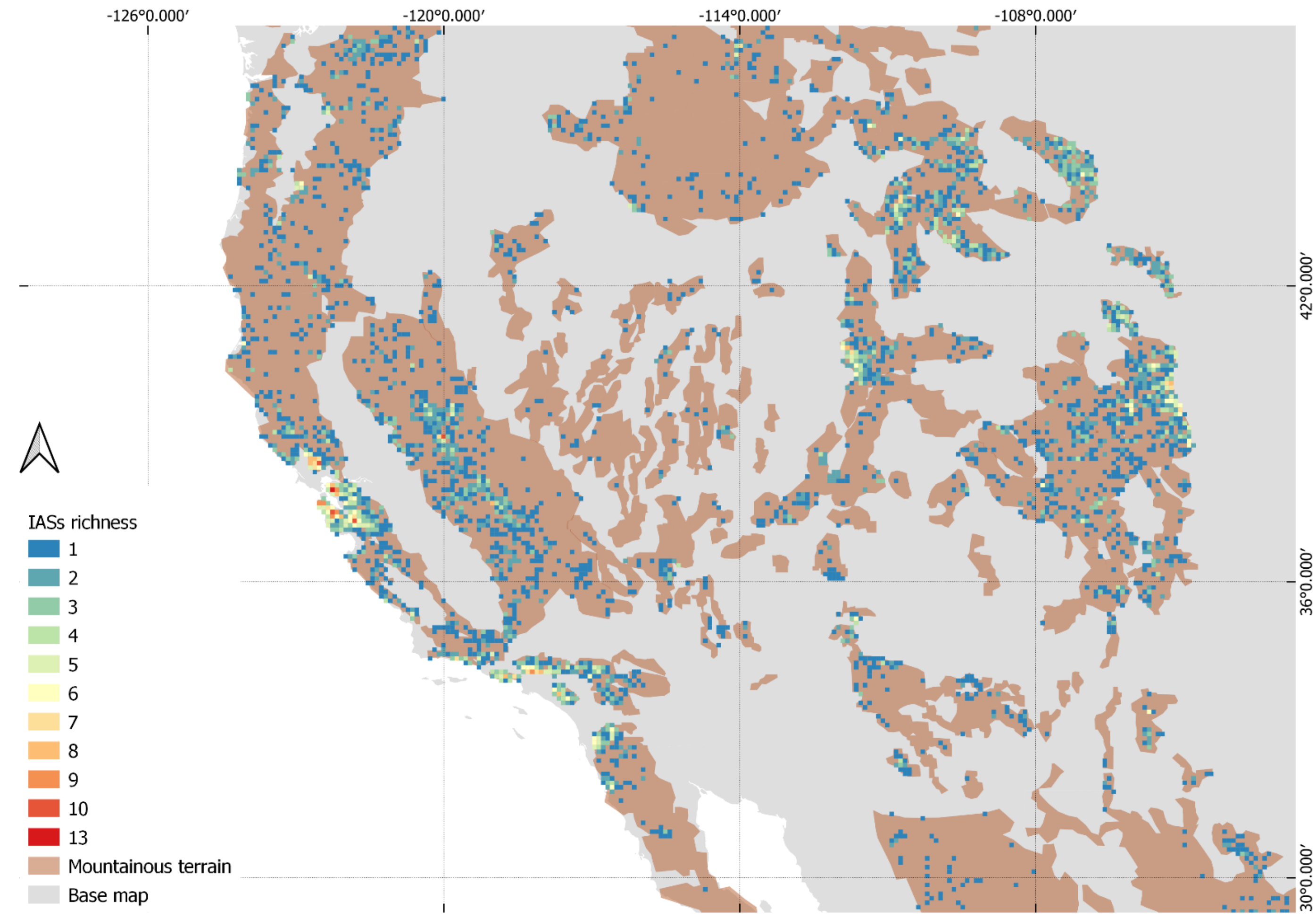


Figure F2. Maps showing IASs richness hotspots in: A) Europe; B) APP (USA, North America); C) Central RM (USA, North America), and D) Taiwan (HIM, China, Asia). Extensions without impact cells represent the areas without IASs occurrence points.






-126°0.000′
-120°0.000′
-114°0.000′
-108°0.000′
42°0.000′
36°0.000′
30°0.000′
IASs richness
1
2
3
4
5
6
7
8
9
10
13
Mountainous terrain
Base map

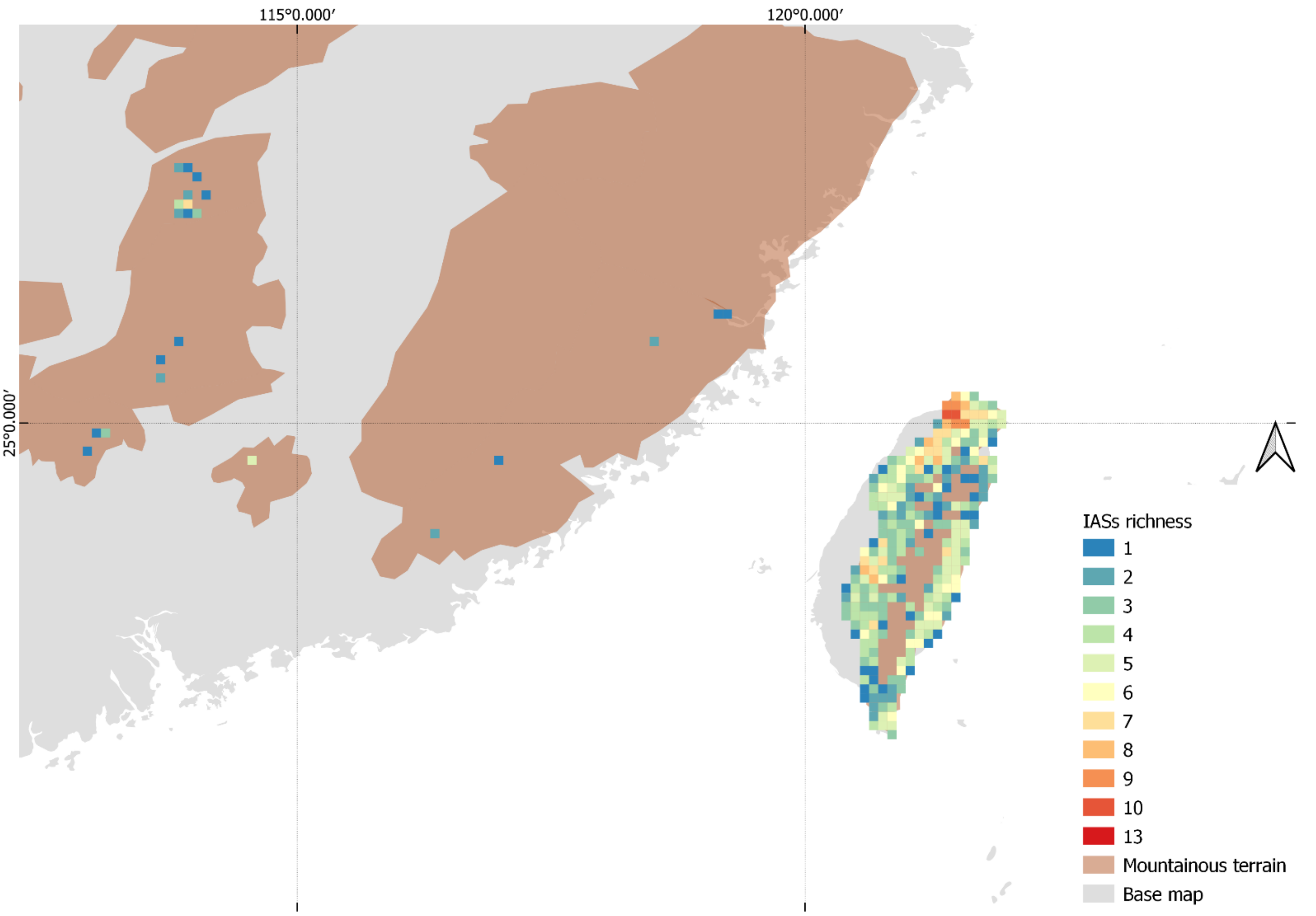

115°0.000′
120°0.000′
25°0.000′
IASs richness
1
2
3
4
5
6
7
8
9
10
13
Mountainous terrain
Base map

Figure F3. Scatterplots showing the relationship between sqrt(StCIMPAL) scores and elevation (in meters) for every GMR. We used SPS1 dataset.

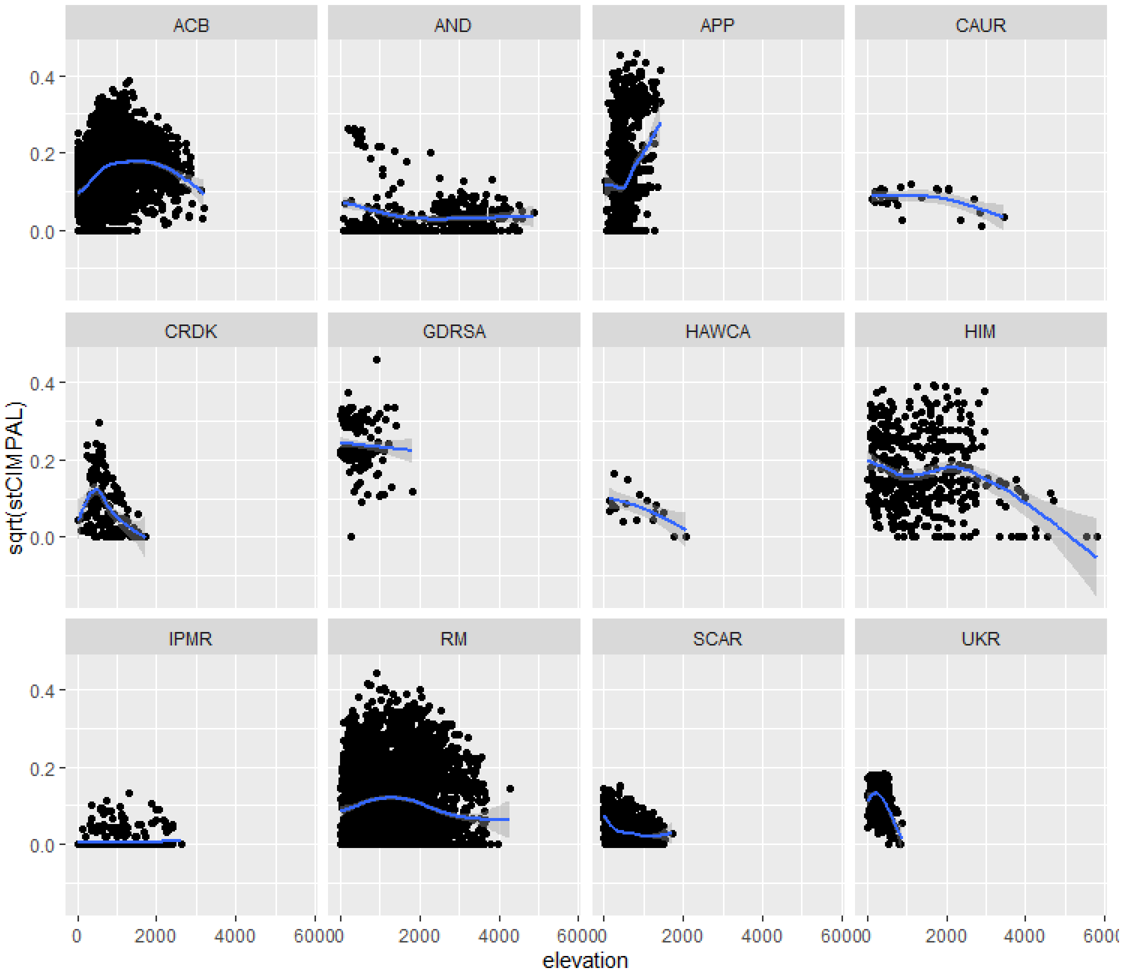


Figure F4. StCIMPAL scores (upper boxplot) and square root transformed StCIMPAL scores (lower boxplot) for each GMR (twelve levels) using SPS1 dataset.

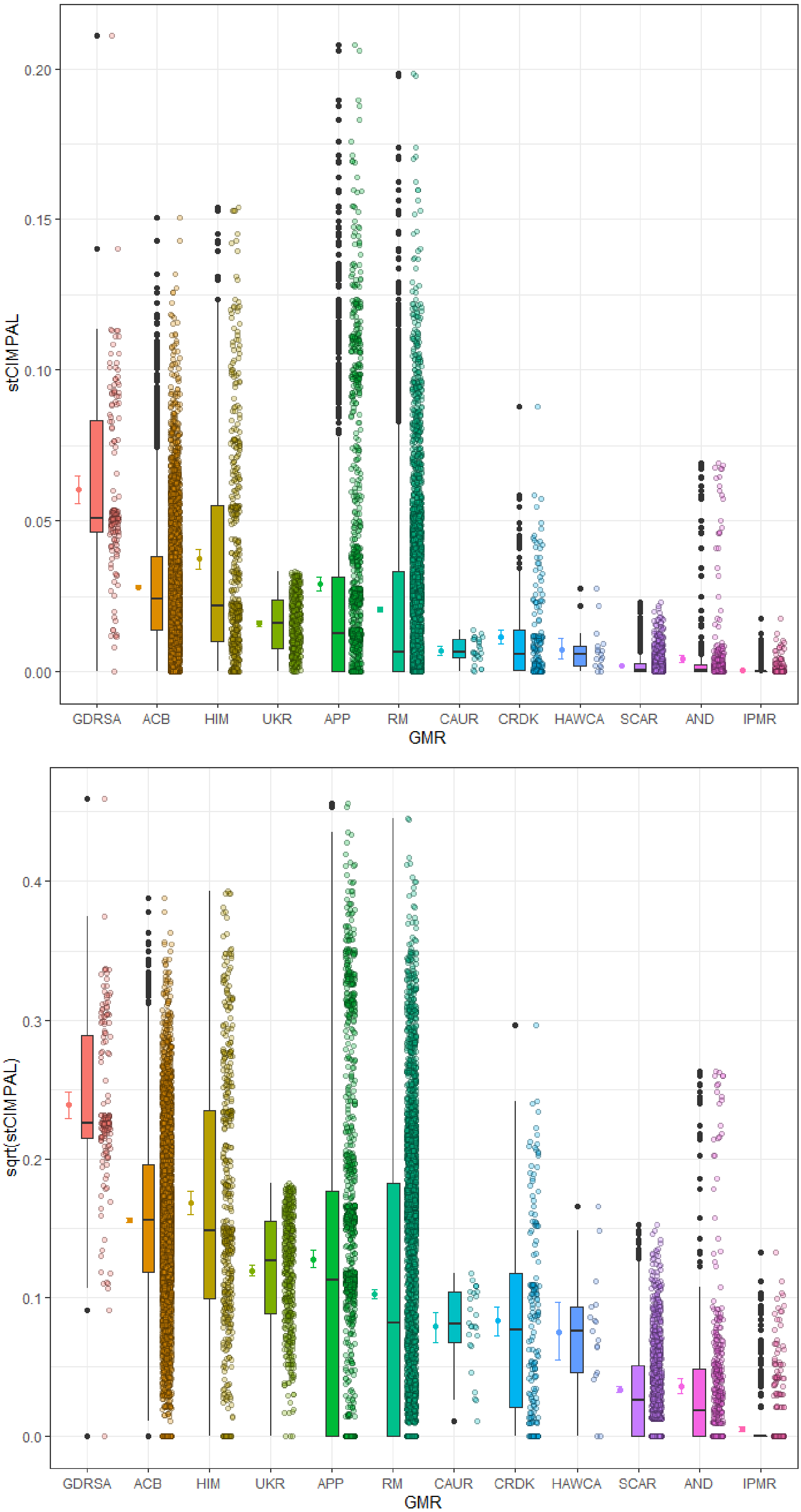


Figure F5. Plot with EMMs as side-by-side CIs and "comparison arrows". Contrast: Animalia – Plantae. Estimate: -0.19. SE: 0.025. df: Inf. Z-ratio: -7.598. *P*-value: <0.0001. Results are averaged over the levels of GMR.

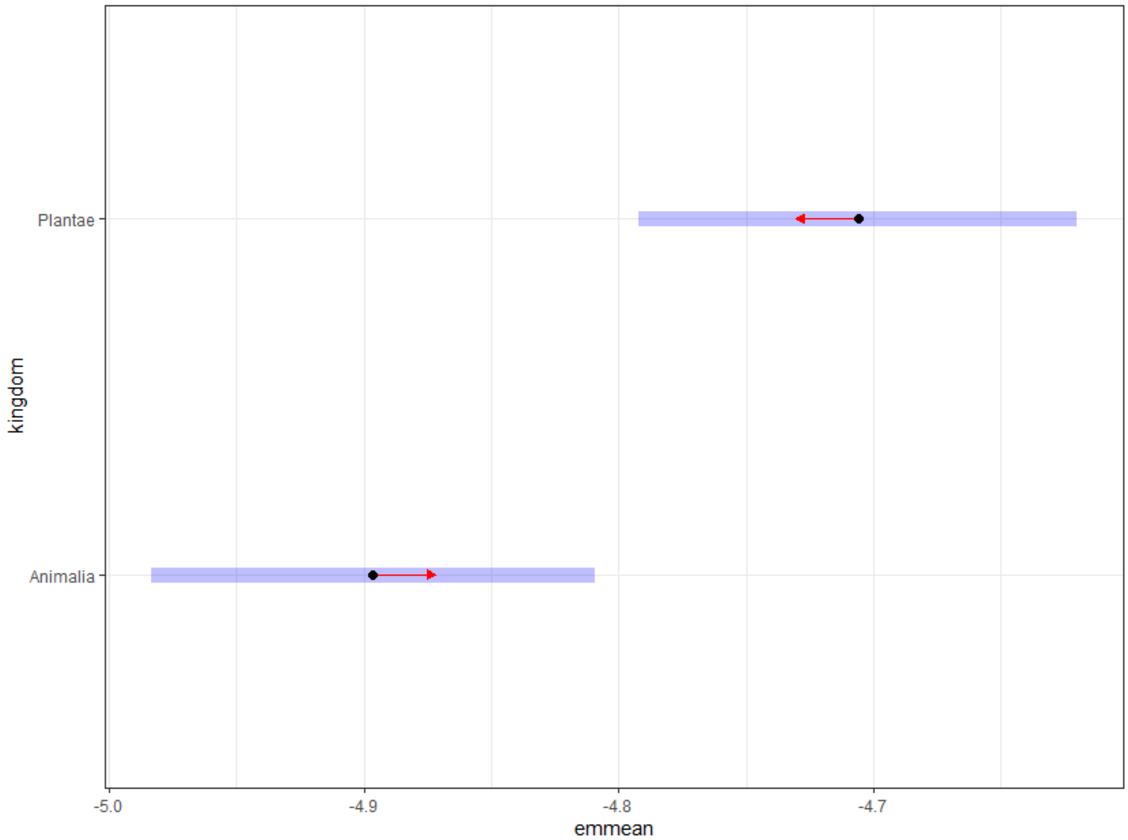
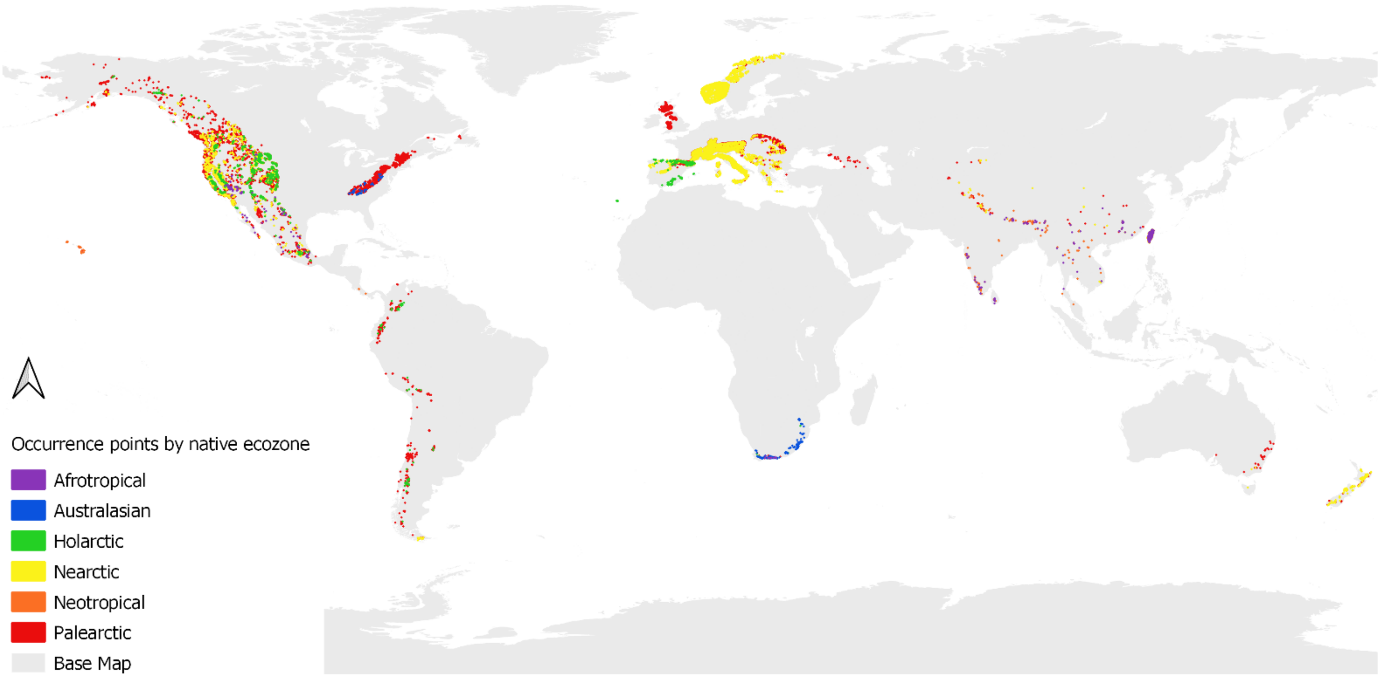
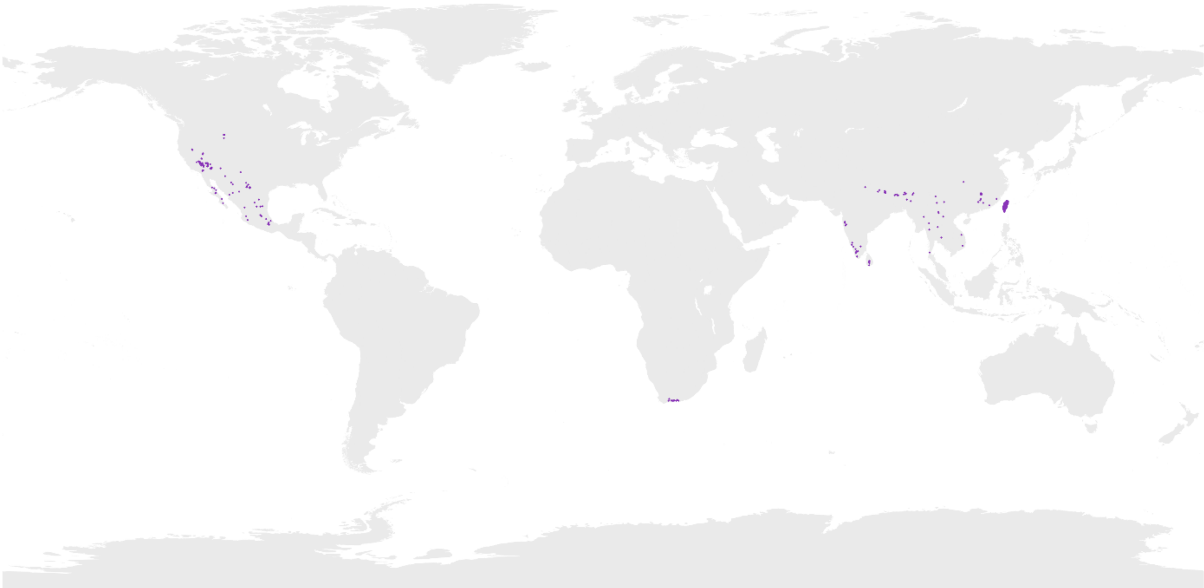
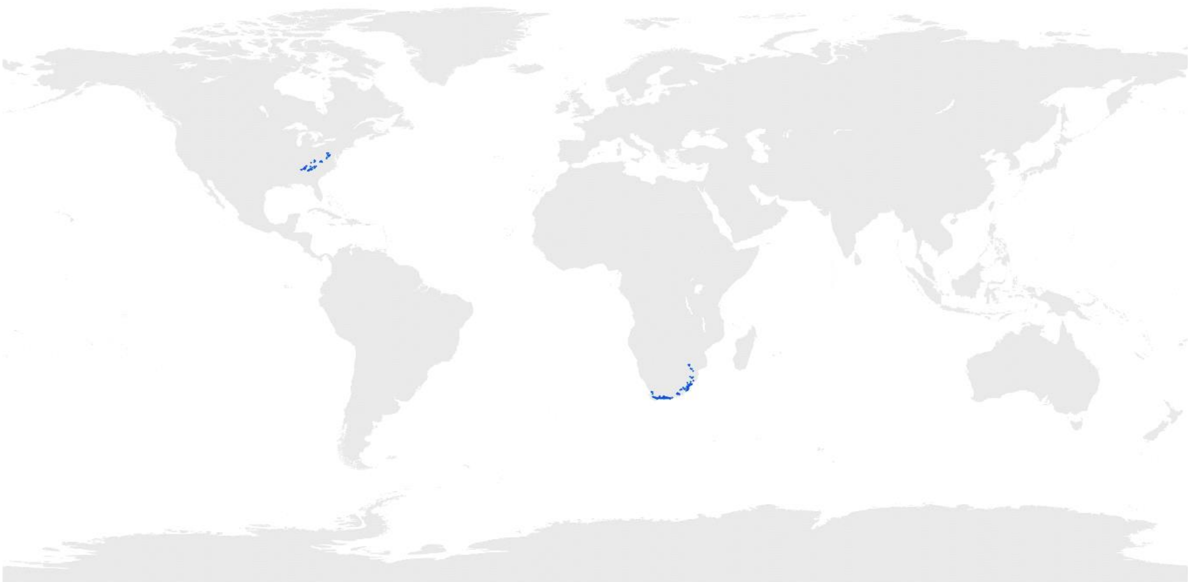
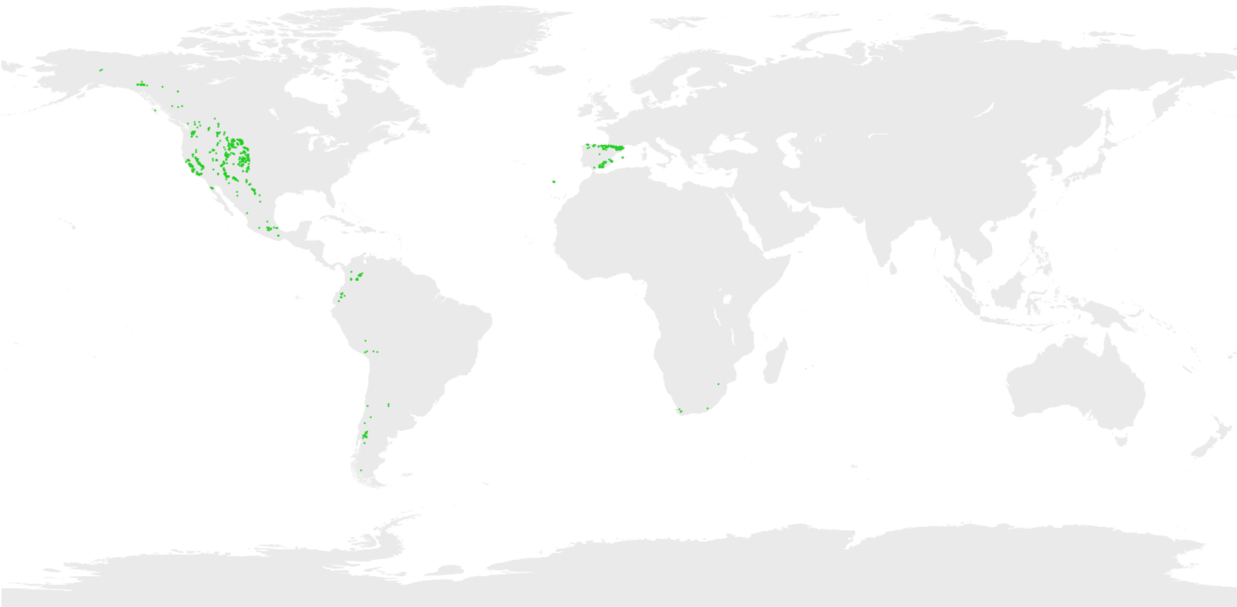


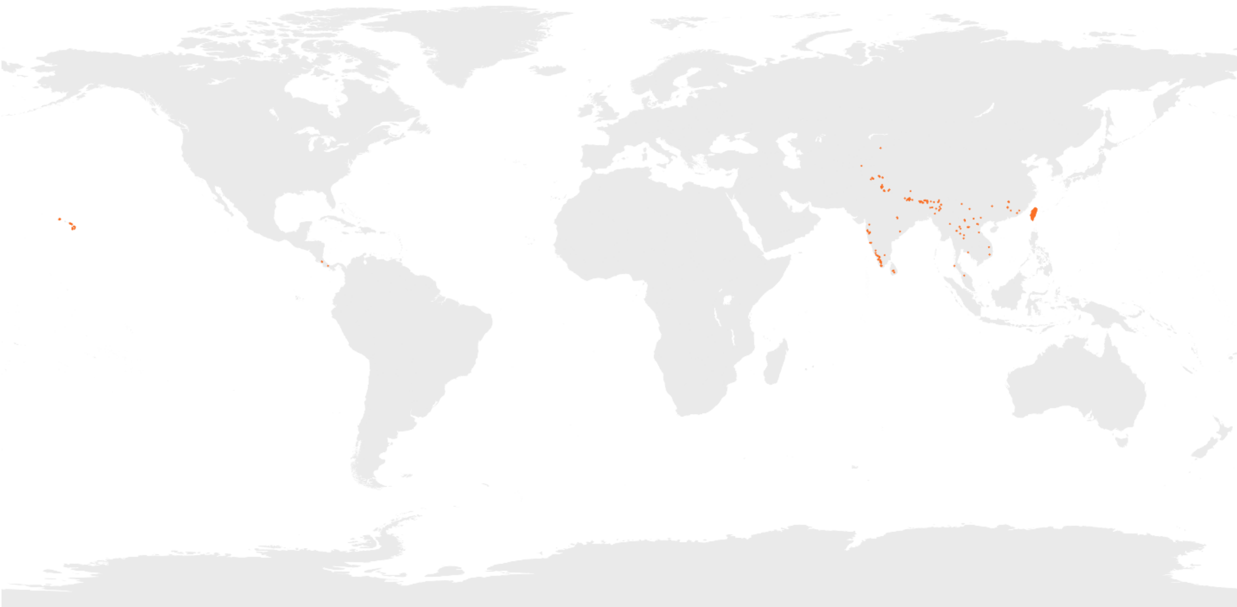
Figure F6. Maps showing IASs occurrence by native ecozone worldwide. Extensions without impact cells represent the areas without IASs occurrence points.











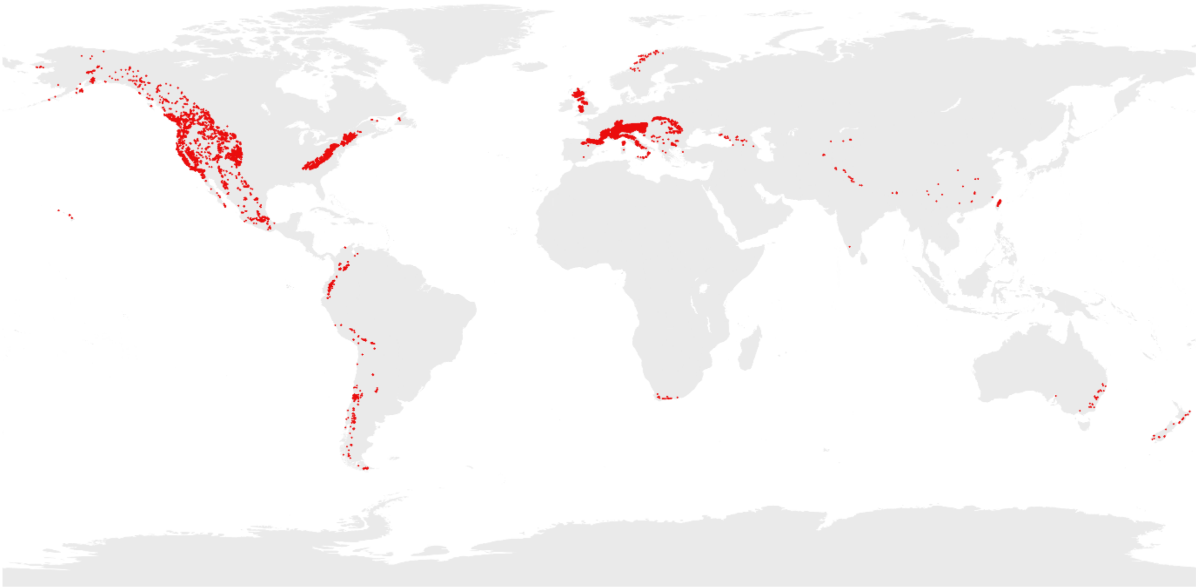


Table F1. Model 2. Estimated regression parameters, standard errors, t values, and P-values for the Tweedie's compound Gamma-Poisson GLM presented in Equation (2). The estimated value for φ and p were 0.157 and 1.505 respectively. Model AIC: -41352. Degrees of freedom: 12429. We used SPS2 dataset.

	Estimate	Std. Error	t value	P-value	
Intercept	-4.478	0.034	-132.202	<2e-16	***
GMRAND	-1.601	0.193	-8.289	<2e-16	***
GMRAPP	-0.294	0.062	-4.716	2e-06	***
GMRCRDK	-1.325	0.188	-7.044	2e-12	***
GMRGDRSA	1.119	0.232	4.826	1e-06	***
GMRHAWCA	-2.168	1.062	-2.041	0.041	*
GMRHIM	-0.523	0.087	-0.609	0.542	
GMRIPMR	-4.556	0.255	-17.876	<2e-16	***
GMRRM	0.174	0.044	3.970	7e-05	***
GMRSCAR	-3.884	0.343	-11.339	<2e-16	***
IASsRichness	0.416	0.014	30.578	<2e-16	***
GMRAND : IASsRichness	0.042	0.130	0.323	0.747	
GMRAPP : IASsRichness	0.166	0.025	6.746	2e-11	***
GMRCRDK : IASsRichness	0.400	0.094	4.238	2e-05	***
GMRGDRSA : IASsRichness	0.084	0.198	0.424	0.671	
GMRHAWCA : IASsRichness	0.922	0.775	1.190	0.234	
GMRHIM : IASsRichness	-0.051	0.023	-2.191	0.029	*
GMRIPMR: IASsRichness	0.140	0.118	1.186	0.236	
GMRRM : IASsRichness	-0.181	0.182	-9.955	<2e-16	***
GMRSCAR : IASsRichness	1.738	0.345	5.348	9e-08	***

Table F2. Model 3. Estimated regression parameters, standard errors, t values, and P-values for the Tweedie's compound Gamma-Poisson GLM presented in Equation (3). The estimated value for φ and p were 0.148 and 1.500 respectively. Model AIC: -41830. Degrees of freedom: 12418. We used SPS2 dataset.

	Estimate	Std. Error	t value	P-value	
Intercept	-4.729	0.046	-104.055	<2e-16	***
GMRAND	-0.311	0.211	-1.477	0.140	
GMRAPP	-0.502	0.085	-5.931	3e-09	***
GMRCRDK	-0.014	0.305	-0.047	0.963	
GMRGDRSA	1.449	0.238	6.101	2e-09	***
GMRHAWCA	-1.036	1.166	-0.889	0.374	
GMRHIM	0.340	0.115	2.963	0.003	**
GMRIPMR	-4.183	0.293	-14.278	<2e-16	***
GMRRM	0.720	0.059	12.148	<2e-16	***
GMRSCAR	-2.528	0.353	-7.160	9e-13	***
Elevation	3e-04	3e-05	7.227	5e-13	***
IASsRichness	0.389	0.015	25.340	<2e-16	***
GMRAND : Elevation	-0.001	8e-05	-12.917	<2e-16	***
GMRAPP : Elevation	7e-04	1e-04	5.917	3e-09	***
GMRCRDK : Elevation	-0.002	3e-04	-5.058	4e-07	***
GMRGDRSA : Elevation	-4e-04	2e-04	-2.115	0.034	*
GMRHAWCA : Elevation	-0.001	7e-04	-1.842	0.066	.
GMRHIM : Elevation	-4e-04	6e-05	-6.417	1e-10	***
GMRIPMR : Elevation	-4e-04	2e-04	-1.748	0.08	.
GMRRM : Elevation	-4e-04	3e-05	-13.051	<2e-16	***
GMRSCAR : Elevation	-0.002	2e-04	-10.114	<2e-16	***
GMRAND : IASsRichness	0.231	0.131	1.762	0.078	.
GMRAPP : IASsRichness	0.145	0.024	6.071	1e-09	***
GMRCRDK : IASsRichness	0.276	0.096	2.864	0.004	**
GMRGDRSA : IASsRichness	0.089	0.188	0.473	0.636	
GMRHAWCA : IASsRichness	0.771	0.752	1.026	0.305	
GMRHIM : IASsRichness	-0.073	0.023	-3.184	0.002	**
GMRIPMR : IASsRichness	0.117	0.118	0.987	0.324	
GMRRM : IASsRichness	-0.210	0.018	-11.840	<2e-16	***
GMRSCAR : IASsRichness	1.402	0.312	4.495	7e-06	***
Elevation : IASsRichness	4e-05	1e-05	4.374	1e-05	***

Table F3. Model 4. Estimated regression parameters, standard errors, t values, and P-values for the Tweedie's compound Gamma-Poisson GLM presented in Equation (4). The estimated value for φ and p were 0.108 and 1.198 respectively. Model AIC: -12425. Degrees of freedom: 12894. We used SPS1 dataset.

	Estimate	Std. Error	t value	P-value	
Intercept	-2.008	0.020	-100.780	< 2e-16	***
GMRAND	-0.860	0.118	-7.271	4e-13	***
GMRAPP	-0.524	0.052	-10.118	< 2e-16	***
GMRCAUR	-0.321	0.258	-1.244	0.213	
GMRCRDK	0.309	0.141	-2.195	0.028	*
GMRGDRSA	0.618	0.078	7.950	2e-15	***
GMRHAWCA	-0.061	0.354	-0.172	0.864	
GMRHIM	0.364	0.053	6.809	1e-11	***
GMRIPMR	-3.625	0.220	-16.485	< 2e-16	***
GMRRM	-0.0979	0.032	-3.090	0.002	**
GMRSCAR	-0.875	0.069	-12.739	< 2e-16	***
GMRUKR	0.161	0.087	1.842	0.065	.
Elevation	2e-04	2e-05	8.966	< 2e-16	***
GMRAND : Elevation	-4e-04	5e-05	-7.243	4e-13	***
GMRAPP : Elevation	7e-04	8e-05	8.745	< 2e-16	***
GMRCAUR : Elevation	-3e-04	2e-04	-1.908	0.056	.
GMRCRDK : Elevation	-1e-04	2e-04	-6.766	1e-11	***
GMRGDRSA : Elevation	-3e-04	1e-04	-1.935	0.053	.
GMRHAWCA : Elevation	-9e-04	4e-04	-2.104	0.0354	*
GMRHIM : Elevation	-3e-04	4e-05	-7.479	8e-14	***
GMRIPMR : Elevation	2e-04	2e-04	1.048	0.295	
GMRRM : Elevation	-3e-04	2e-05	-11.948	< 2e-16	***
GMRSCAR : Elevation	-0.001	1e-04	-9.962	< 2e-16	***
GMRUKR : Elevation	-0.001	3e-04	-4.178	3e-05	***

Table F4. Model 5. Estimated regression parameters, standard errors, t values, and P-values for the Tweedie's compound Gamma-Poisson GLM presented in Equation (5). The estimated value for φ and p were 0.094 and 1.179 respectively. Model AIC: -12699. Degrees of freedom: 12429. We used SPS2 dataset.

	Estimate	Std. Error	t value	P-value	
Intercept	-2.311	0.021	-112.562	< 2e-16	***
GMRAND	-1.621	0.128	-12.673	< 2e-16	***
GMRAPP	-0.522	0.040	-13.023	< 2e-16	***
GMRCRDK	-0.900	0.117	-7.693	2e-14	***
GMRGDRSA	-0.600	0.147	4.082	4e-05	***
GMRHAWCA	-1.214	0.625	-1.943	0.052	.
GMRHIM	-0.068	0.053	-1.288	0.198	
GMRIPMR	-3.663	0.210	-17.487	< 2e-16	***
GMRRM	-0.274	0.028	-9.886	< 2e-16	***
GMRSCAR	-2.500	0.202	-12.375	< 2e-16	***
IASsRichness	0.221	0.008	26.357	< 2e-16	***
GMRAND : IASsRichness	0.237	0.081	2.925	0.004	**
GMRAPP : IASsRichness	0.171	0.016	11.002	< 2e-16	***
GMRCRDK : IASsRichness	0.262	0.059	4.433	9e-06	***
GMRGDRSA : IASsRichness	0.034	0.126	0.269	0.788	
GMRHAWCA : IASsRichness	0.531	0.459	1.160	0.246	
GMRHIM : IASsRichness	-0.022	0.015	-1.507	0.132	
GMRIPMR: IASsRichness	0.177	0.095	1.863	0.063	
GMRRM : IASsRichness	-0.047	0.011	-4.089	4e-05	***
GMRSCAR : IASsRichness	1.169	0.191	6.122	1e-09	***

Table F5. Model 6. Estimated regression parameters, standard errors, t values, and P-values for the Tweedie's compound Gamma-Poisson GLM presented in Equation (6). The estimated value for φ and p were 0.091 and 1.175 respectively. Model AIC: -13011. Degrees of freedom: 12418. We used SPS2 dataset.

	Estimate	Std. Error	t value	P-value	
Intercept	-2.441	0.028	-85.820	< 2e-16	***
GMRAND	-0.944	0.146	-6.481	9e-11	***
GMRAPP	-0.650	0.056	-11.607	< 2e-16	***
GMRCRDK	-0.044	0.194	-0.225	0.822	
GMRGDRSA	0.790	0.155	5.091	4e-07	***
GMRHAWCA	-0.470	0.696	-0.676	0.499	
GMRHIM	0.210	0.072	2.855	0.004	**
GMRIPMR	-3.591	0.248	-14.475	< 2e-16	***
GMRRM	0.082	0.039	2.117	0.034	*
GMRSCAR	-1.635	0.215	-7.592	3e-14	***
Elevation	1e-04	2e-05	6.011	2e-09	***
IASsRichness	0.200	0.010	20.286	< 2e-16	***
GMRAND : Elevation	-4e-04	5e-05	-8.382	< 2e-16	***
GMRAPP : Elevation	4e-04	7e-05	5.385	7e-08	***
GMRCRDK : Elevation	-0.001	2e-04	-5.132	3e-07	***
GMRGDRSA : Elevation	-3e-04	1e-04	-2.052	0.040	*
GMRHAWCA : Elevation	-8e-04	4e-04	-2.032	0.042	*
GMRHIM : Elevation	-2e-04	4e-05	-6.722	2e-11	***
GMRIPMR : Elevation	-2e-05	2e-04	-0.117	0.907	
GMRRM : Elevation	-3e-04	2e-05	-12.763	< 2e-16	***
GMRSCAR : Elevation	-0.001	1e-04	-9.659	< 2e-16	***
GMRAND : IASsRichness	0.272	0.082	3.334	0.001	***
GMRAPP : IASsRichness	0158	0.016	10.188	< 2e-16	***
GMRCRDK : IASsRichness	0.179	0.062	2.889	0.004	**
GMRGDRSA : IASsRichness	0.040	0.124	0.321	0.749	
GMRHAWCA : IASsRichness	0.447	0.454	0.985	0.325	
GMRHIM : IASsRichness	-0.037	0.015	-2.502	0.012	*
GMRIPMR : IASsRichness	0.127	0.097	1.297	0.195	
GMRRM : IASsRichness	-0.065	0.011	-5.682	1e-08	***
GMRSCAR : IASsRichness	0.931	0.190	4.99	9e-07	***
Elevation : IASsRichness	3e-05	6e-06	4.737	2e-06	***

Table F6. Pairwise comparisons using Wilcoxon rank sum test with continuity correction. *P*-value adjustment method: Bonferroni. ****: $P \leq 0.0001$; ***: $P \leq 0.001$; **: $P \leq 0.01$; ns: $P > 0.05$.

GMR	ACB	AND	APP	CAUR	CRDK	GDRSA	HAWCA	HIM	IPMR	RM	SCAR
AND	****										
APP	****	****									
CAUR	****	****	ns								
CRDK	****	****	**	ns							
GDRSA	****	****	****	****	****						
HAWCA	****	**	ns	ns	ns	****					
HIM	ns	****	****	****	****	****	**				
IPMR	****	****	****	****	****	****	****	****			
RM	****	****	****	ns	ns	****	ns	****	****		
SCAR	****	ns	****	****	****	****	**	****	****	****	
UKR	****	****	ns	***	****	****	**	****	****	****	****

Table F7. Model 7. Estimated regression parameters, standard errors, t values, and *P*-values for the Tweedie's compound Gamma-Poisson GLM presented in Equation (7). The estimated value for φ and p were 0.1481 and 1.500 respectively. Model AIC: -86625. Degrees of freedom: 23786. The model' residues could be better fitted, and therefore it is necessary to conduct more analysis to find a more suitable model.

	Estimate	Std. Error	t value	P-value	
Intercept	-4.422	0.028	-157.617	< 2e-16	***
GMRAND	-1.287	0.080	-15.991	< 2e-16	***
GMRAPP	0.253	0.031	8.276	< 2e-16	***
GMRCAUR	-0.556	0.287	-1.941	0.052	.
GMRCRDK	-0.502	0.092	-5.448	5e-08	***
GMRGDRSA	1.387	0.068	20.472	< 2e-16	***
GMRHAWCA	-0.817	0.276	-2.961	0.003	**
GMRHIM	-0.048	0.038	-1.272	0.203	
GMRIPMR	-3.392	0.096	-35.313	< 2e-16	***
GMRRM	-0.047	0.024	-1.943	0.052	.
GMRSCAR	-1.000	0.053	-18.775	< 2e-16	***
GMRUKR	0.317	0.062	5.126	3e-07	***
Kingdom Plantae	0.190	0.025	7.598	3e-14	***

Table F8. Model 8. Estimated regression parameters, standard errors, t values, and *P*-values for the Tweedie's compound Gamma-Poisson GLM presented in Equation (8). The estimated value for φ and p were 0.144 and 1.497 respectively. Model AIC: -86973. Degrees of freedom: 23782. The model' residues could be better fitted, and therefore it is necessary to conduct more analysis to find a more suitable model.

	Estimate	Std. Error	t value	P-value	
Intercept	-3.835	0.070	-54.616	< 2e-16	***
Australasian	0.223	0.141	1.582	0.114	
Holarctic	0.281	0.079	3.566	3e-04	***
Nearctic	-0.439	0.070	-6.324	3e-10	***
Neotropical	-0.525	0.076	-6.906	5e-12	***
Palearctic	-0.374	0.070	-5.353	9e-08	***
GMRAND	-1.438	0.076	-18.950	< 2e-16	***
GMRAPP	0.121	0.029	4.199	3e-05	***
GMRCAUR	-0.769	0.268	-2.865	0.004	**
GMRCRDK	-1.017	0.138	-7.399	1e-13	***
GMRGDRSA	1.342	0.064	20.958	< 2e-16	***
GMRHAWCA	-0.785	0.266	-2.950	0.003	**
GMRHIM	-0.070	0.056	-1.250	0.211	
GMRIPMR	-3.776	0.090	-42.204	< 2e-16	***
GMRRM	-0.245	0.021	-12.001	< 2e-16	***
GMRSCAR	-1.151	0.046	-24.859	< 2e-16	***
GMRUKR	0.104	0.054	1.935	0.053	.

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Erratum

Upon completion of the MSc thesis titled "*Mapping the impact of invasive alien species on mountain ecosystems*", authored by the student Joan Rabassa-Juvanteny and supervised by Dr. Bernat Claramunt-López, certain typographical errors and minor wording adjustments were identified in the supplementary materials of the submitted version. The main text is free of errors, though formatting and the cross-referencing of appendices could be refined. The specific corrections in the supplementary materials are detailed below:

Main Text

No errors were found.

Supplementary Materials and Data

- **Appendix A (Appendix A7):**
    - Figure A7.1 (change 6 to 7), pg. 4 of Supplementary Materials.
    - Figure A7.2 (change 6 to 7), pg. 4 of Supplementary Materials.
- **Appendix E:**
    - **Specific considerations** → **Group A** → taxa (replace "rates"), pg. 22 of Supplementary Materials.
    - Table E1 (in two rows) → Look (replace "Loot"), on pg. 27 of Supplementary Materials.
- **Appendix F:**
    - Appendix F is not explicitly mentioned in the Main Text.

And to certify this, I sign this erratum in Bellaterra, on November 6, 2024.

Joan Rabassa-Juvanteny